### (FILE 'HOME' ENTERED AT 16:14:42 ON 21 JUN 2004)

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FILE 'MEDLINE, BIOSIS, SCISEARCH, BIOTECHDS, CAPLUS' ENTERED AT 16:15:02
     ON 21 JUN 2004
L1
          35108 S TYROSINE(W) PHOSPHATASE# OR PTP# OR PTPR#
L2
           2424 S PLOWMAN?/AU
L3
             17 S L1 AND L2
L4
              9 DUP REM L3 (8 DUPLICATES REMOVED)
L5
              0 S BAHIJA?/AU
L6
             81 S PTP5 OR (PTP(W)5) OR PTP05
L7
             78 S L6 AND PY<1998
\Gamma8
             49 DUP REM L7 (29 DUPLICATES REMOVED)
L9
           7607 S L1 AND (ADIPOSE OR FAT OR HEMATOPOIETIC OR HAEMATOPOIETIC OR
           1750 S L1(5A) (HEMATOPOIETIC OR HAEMATOPOIETIC OR (T OR B OR NK) (W) (C
L10
L11
             48 S L1(5A) (FAT OR ADIPOSE)
L12
             18 S L11 AND PY<1998
L13
             12 DUP REM L12 (6 DUPLICATES REMOVED)
     FILE 'PCTFULL, USPATFULL, EUROPATFULL' ENTERED AT 17:11:43 ON 21 JUN 2004
L14
           8955 S TYROSINE(W) PHOSPHATASE# OR PTP#
L15
             16 S L14(5A) (FAT OR ADIPOSE)
L16
            468 S L14/TI,AB
L17
            151 S L16 AND (FAT OR ADIPOSE)
L18
              8 S L17 AND PD<19970611
L19
            948 S L14 AND ADIPOSE
L20
            117 S L14(S)ADIPOSE
L21
              0 S L20 AND PD<19970611
L22
              2 S L20 AND AD<19970611
     FILE 'MEDLINE' ENTERED AT 17:24:29 ON 21 JUN 2004
L23
              1 S (95 AND 2806 AND 1995)/SO
     FILE 'STNGUIDE' ENTERED AT 17:26:04 ON 21 JUN 2004
     FILE 'MEDLINE, BIOSIS, SCISEARCH, CANCERLIT, LIFESCI, BIOTECHDS, CAPLUS'
     ENTERED AT 17:26:29 ON 21 JUN 2004
            172 S L1(S) (FAT OR ADIPOSE)
L24
L25
          40615 S TYROSINE(W) PHOSPHATASE# OR PTP# OR PTPR#
L26
            115 S L25(S)ADIPOSE
L27
             38 S L26 AND PY<1998
L28
             19 DUP REM L27 (19 DUPLICATES REMOVED)
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Minimum
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2439
1 MSSPRKVRGKTGRDNDEEEG.....QYQFCYEIVLEVLQNLLALY 463
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2439 2212.5 2210.5 2104.5 1378.5 1399.5 1306 1306 1306.5 1306.5 1307.5 639.5 639.5 639.5 639.5 639.5 639.5 639.5	Score
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AAW89250 AAW89249 AAW89249 AAW89251 AAB14454 ABE08106 ABG08045 ABG08045 ADB09795 ADB09795 ADB09795 ADB09795 AAB37996 AAAB37994 AAG67637 AAG67637 AAG67637 AAG67637 AAG67637 AAG67937 AAG790272 AAB19343 AAW790272 AAW12522 AAW25156 AAW25156 AAW25156 AAW25333 ADD18742 AAG79333 ADD18742	SUMMARIES ID
Aaw89250 Mouse PTP Aaw89249 Mouse PTP Aaw89249 Mouse PTP Aaw89251 Mouse PTP Aae14454 Human pro Ade001106 Novel pro Ade001106 Novel pro Ade09123 Novel pro Ade97994 Human DKF Ad6897995 Human Kin Aae37996 Human kin Aae37996 Human kin Aae379368 Human pro Aaw75999 Intracell Aay90272 Human pro Aaw89252 Protein Aaw89252 Rat PTP10 Aaw1522 Protein Aay7933 PTPH1. 8/ Add18742 Human pro Add18744 Human pro Add18744 Human pro	Description

The present invention describes isolated, acids encoding PTP04, SAD, PTP05, PTP10, F present sequence represent mouse PTP05 at NLK-7, are protein tyrosine phosphatases

ALP and ALK-7 proteins. The The above proteins, other than (PTPs) and are used to identify

Claim 2;

Page

157-158; 193pp; English.

New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.

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## ALIGNMENTS

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20-MAY-1997;
11-JUN-1997;
11-JUN-1997;
18-JUN-1997;
23-OCT-1997;
                                                                                                                                                                                                                                                 PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphom neurodegenerative disease; neuronal survival; Alzheimer's disease; parkinson's disease;
                                                                              WPI; 1999-009434/01.
N-PSDB; AAV81745.
                                                                                                   Plowman GD,
Courtneidge
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SA, App
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                                                                                                             PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphom neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease.
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The present invention describes isolated, enriched or purified nucleic colds encoding PTP04, SAD, PTP05, PTP05, ALP and ALK-7 proteins. The CC acids encoding PTP04, SAD, PTP05, PTP05. The above proteins. The CALK-7, are protein tyrosine phosphatases (PTP05) and are used to identify CC substances that modulate their activity (i.e. agonists and antagonists, CC including NBP) in vivo or in vitro. These substances are used to treat or CC prevent diseases associated with abnormal signal transduction pathways CC that involve the proteins, particularly cancer (e.g. leukaemia and CC lymphoma), while modulators of ALK-7 (which is a type I receptor CC serine/threonine kinase) are used to promote neuronal survival, CC particularly for treating Alzheimer's, Parkinson's or Huntington's CC diseases. Nucleic acid fragments of the polymucleotides encoding the CC proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene corrections.
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20-MAY-1997;
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18-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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Courtneidge SA,
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RESULT 3
AAW89251
ID AAW89251
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AXC A
                                                                                                                                                                        CC The present invention describes isolated, enriched or purified nucleic cacids encoding PTP04, SAD, PTP05, PTP104, ALP and ALK-7 proteins. The present sequence represents mouse PTP05. The above proteins, other than CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, CC including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and CC lymphoma), while codulators of ALK-7 (which is a type I receptor CC serine/threonine kinase) are used to promote neuronal survival, CC particularly for treating Alzheimer's, Parkinson's or Huntington's CC diseases. Nucleic acid fragments of the polynucleotides encoding the groteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene transpy (optionally after mutation). Ab are used to determine the
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  Query Match
Best Local Similarity
Matches 405; Conserv
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20-MAY-1997;
11-JUN-1997;
11-JUN-1997;
11-JUN-1997;
18-JUN-1997;
                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding specific protein tyrosine phosphatases - for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.
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Courtneidge
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Pred. No. 4.1e-193;
D; Mismatches 0;
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16-JUN-2000;
22-JUN-2000;
29-JUN-2000;
06-JUL-2000;
12-JUL-2000;
                                                                                                                                                                                                                                                                      Human; protein phosphatase; PP-4; immune system disorder; AIDS; allergy; neurological disorder; developmental disorder; Alzheimer's disease; cell proliferative disorder; Huntington's disease; arteriosclerosis; renal tubular acidosis; gonadal dysgenesis; cancer; ademocarcinoma; leukaemia; transgenic animal; gene therapy.
                                                                                                                                            Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               such as Down's syndrome, cerebral palsy, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder such as akathesia, ammesia, catationia, dyskinesia; developmental disorders include e.g. renal tubular acidosis, Ducheme and Becker muscular dystrophy, gonadal dysgenesis, hypothyroidism; cell proliferative disorders include e.g. actinic keratosis, arteriosclerosis, currinosis, hepatitis, psoriasis and cancer cincluding adenocarcinoma, leukaemia. The polypeptide and polynucleotide are further useful for analysing proteome of a tissue or a cell type, for screening an agonist/antagonist, a compound that specifically binds to it or its modulator. The polynucleotide is useful for creating knockin humanised animals (pigs) or transgenic animals (mice or rate) to model type, which represents the global pattern of gene expression by a concern.
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Best Local S
Matches 274
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Hafalia A, Keu
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Ramkumar J, Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is human protein phosphatase (PP)-4. Pp polymucleotide and polypoptide are useful in the diagnosis, treatment prevention of immune system disorders, neurological disorders, developmental disorders and cell proliferative disorders. Examples of immune system disorders and cell proliferative disorders. Examples of immune system disorders include acquired immune deficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 105-106; 116pp;
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                                                                                                                                                                                                                                         VFLLIKTIWYNVFKLWKGKLIFGNKWNSENVKPSHHLSFSDKYELVYPBPLESDTDETVW
                                                                                                                                                                                                                                                                                                            MSSPRKVRGKTGRDNDEEEGNSGNLNLRNSLPSSSQKMTPTKPVQNKNLMKYEEHLDILM
                                                                           SSARSAMRDCLNTLQKK-EELDIIREFLELEQMTLPDDFNSGNTLQNRDKNRYRDILPYD
                                                                                                                                                                                                                                                                                  MSSPRDFRAEPVNDYEGNDSEAEDLNFRETLPSSSQENTPRSKV-
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, Reddy R, Sa
CM, Walia NK,
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENOMICS
                                                                                                                                                                                                                                                                                                                                                                                   59.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Ding L, Elliott VS, Gandhi AR,
Lee EA, Lu Y, Nguyen DB, Pattez
Sanjanwala MS, Stewart EA, Tang Y
K, Yang J, Yao MG, Yue H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INC
                                                                                                                                                                                                                                                                                                                                                                 52;
                                                                                                                                                                                                                                                                                                                                                               Score 1378.5; DB 5;
Pred. No. 2.7e-123;
2; Mismatches 92;
                                                                                                                                                                                                   PENKVNSEKVKLSLRNFPHNDYEDVFEEPSESGSDPSMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
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Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                          420;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-DEC-2001;
11-DEC-2001;
14-MAR-2002;
                                                       expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT,
Ghosh M,
                                                                                                                                                                                                                                                                                                                                        New polynucleotides, useful for expressing recombinant proteins analysis, characterization or therapeutic use, or as markers for in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                     proteins. The markers for
                                                                                                                                                                                                                                          The invention
                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 1172; 1177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAR-2002;
12-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-DEC-2002; 2002WO-US039555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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)B; ADE07195.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSFNIMDIVAQMREQRSGMVQTKEQYHFCYDIVLEVLRKLLTL 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQNLLLAL 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QPTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIBGGIIKCYHYWPISLKKPLELKHPRVPLENYQILQYFIIRMPQVVEKSTGTSHSVKQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Asundi V, Goodrich RW, Ren F, Zhang
Xue AJ, Wehrman T, Weng G, Zhou P,
ng D, Chen R, Xu C, Boyle BJ;
                                                                                                                                                                                                              The DNA and
                                                                                                                                                                               on comprises the amino acid and coding sequences of novel he DNA and protein sequences of the invention are useful as: tissues in which the corresponding protein is preferentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2002US-0365384P.
; 2002US-0372381P.
; 2002US-0372615P.
; 2002US-00128558.
; 2002US-0376045P.
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2001US-0339453P.
2002US-0365091P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang J;
Wang Z;
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Sequence 508 AA;

Score

1345;

BB 7;

Length 508;

Similarity

58.5%

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RESULT 6
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Matches 27
                                                               New isolated polymucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                    biodiversity.
                                                                                                                                                                                                                                                                Drmanac
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23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-0CT-2001
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                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n; chromosome mapping; gene mapping; gene therapy; forensic
supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                         2001-639362/73
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                                                                                                                                                                                                                                                          Liu C,
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2; Mismatches 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated polynucleotide (I) and polypeptide (II) C sequences. (I) is useful as hybridisation probes, polymerase chain CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, CC and in recombinant production of (II). The polynucleotides are also used Ci in diagnostics as expressed sequence tags for identifying expressed equence (II) is useful in gene therapy techniques to restore normal C constitution of (II) or to treat disease states involving (II). (II) is C useful for generating antibodies against it, detecting or quantitating a CC polypeptide in tissue, as molecular weight markers and as a food CC supplement. (II) and its binding partners are useful in medical imaging C of sites expressing (II). (I) and (II) are useful for treating disorders (involving aberrant protein expression or biological activity. The CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and C amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic c patent did not appear in the printed specification, but was obtained in CC electronic format directly from MIPO at semino, in rimh/published not seminoces.
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Best Local Sim
Matches 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 561 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                         NYSFDIMNIVTOMRKORCGMIQTKEQYQFCYEIVLEVLQNLLAL
                                                                           LOPTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEK 418
DCSFNIMDIVAQMREQRSGMVQTKEQYHFCYDIVLEVLRKLLTL
                                                                                                                                                                                                                                      DSTRVELGKSKDYINASYIRIVNCGEEYFYIATQGPLLSTIDDFWQMVLENKSNVIAMIT
                                                                                                                                                                                                                                                               DSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQMVLENNCNVIAMIT
                                                                                                                                                                                                                                                                                                                                              NSSARSAMRDCLNTLQKK-BELDIIRBFLELEQMTLPDDFNSGNTLQNRDKNRYRDILPY
                                                                                                                                                                                                                                                                                                                                                                                              TARGPFREDEWSSEDEEAAGPSQALSPILS------DTRKIVSEGELDQLAQIRPLIF
                                                                                                                                                                                                                                                                                                                                                                                                                                  WDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQDNEGPGGSCAVRASCFLWEPYSGR------VAEQQHASILLPLSIAIPCCI
                                                                                                                                                        REMEGGIIKCYHYWPISLKKPLELKHFRVFLENYQILQYFIIRMFQVVEKSTGTSHSVKQ
                                                                                                                                                                                              REIECGVIKCYSYWPISIKEPLEFEHFSVFLETFHVTQYFTVRVFQIVKKSTGKSQCVKH
                                                                                                                                                                                                                                                                                                                   NFHEQTALKDCLKILEEKTAAYDIMOBFMALELKNIPGEFYSGNOPSNREKNRYRDILPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSNHKTQWLKATIMNLAHDS-VFENKVNSEKVKLSLRNFPHNDYEDVFEEPSESGSDPSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----KTIWY--NVFKLWKGKLIFGNKWNSENVKPSHHLSFSDKYBLVYPEPLESDTDETV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.7%; Score 1309.5; DB 4; 57.3%; Pred. No. 1.8e-116; tive 59; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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RESULT 7
ABG30845
ID ABG3
XX
AC ABG3
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AC ABG3
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AC Huma
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DT 21-0
XX
DE Huma
XX
Huma
                   Human tyrosine phosphatase protein #1
                                         21-OCT-2002
                                                               ABG30845
                                                                                  ABG30845
                                                                                  standard;
                                         (first entry)
                                                                                 protein;
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Human; tyrosine phosphatase; obesity; diabetes; Parkinson's disease;

Claim

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36401; 103pp;

English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC such as obesity, diabetes, a central nervous system (CNS) disorder, CC chronic obstructive pulmonary disease, cardiovascular disorder or cancer. The invention is useful for treating a human tyrosine phosphatase convention is useful for treating the above mentioned disorders. The invention is useful for treating the above mentioned disorders, where the convention is selected from Parkinson's disease, multiple sclerosis, conventions, alzheimer's disease, and Huntington's disease, and the cardiovascular disorder is selected from congestive heart failure and convocatial infarction. The molecules of the invention are useful in congestive assays for detecting diseases and abnormalities or susceptibility to disease and abnormalities related to the presence of cutations in the polypucleotide coding the polypeptide of the invention. The present amino acid sequence represents the human tyrosine phosphatase construction. This sequence is encoded by the human construction.
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human tyrosine phosphatase polypeptide, the regulation of which useful for treating obesity, diabetes, cardiovascular or central ner system disorder, chronic obstructive pulmonary disease and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a new human tyrosine phosphatase polypeptide. The invention is useful for the preparation of a medicame: for modulating the activity of human tyrosine phosphatase in a disease such as obesity, diabetes, a central nervous system (CNS) disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; Fig 2; 145pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      central nervous system disorder; CNS; cardiovascular disorder; stroke; chronic obstructive pulmonary disease; cancer; multiple sclerosis; Alzheimer's disease; Huntington's disease; congestive heart failure;
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DB; ABK89178.
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                                                                                               VMHEEEYFYIATQGPLPETIEDFWQWYLENNCNVIAMITREIECGVIKCYSYWPISLKEP
                                                                                                                                                      YDIMQEFMALELKNI.PGEFYSGNQPSNREKNRYRDII.PYDSTRVPI.GKSKDYINASYIRI
                                                                                                                                                                                 LDIIRBFLELEQWTLPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphatase gene located on chromosome
LELKHFRVFLENYQILQYFIIRMFQVVEKSTGTSHSVKQLQFTKWPDHGTPASADSFIKY
                                 LEFEHFSVFLETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKY
                                                                                                                                                                                                                                                                            PSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQKK-EE
                                                                                                                                                                                                                                                                                                                VFENKVNSEKVKLSLRNFPHNDYEDVFEEPSESGSDPSMWTARGPFRRDRWSSEDEBAAG
                                                                          VNCGEEYPY IATQGPLLSTIDDFWQMVLENNSNVIAMITREMEGGIIKCYHYWPISLKKP
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                    -DTRKIVSEGELDQLAQIRPLIFNFHEQTAIKDCLKILEEKTAA
                                                                                                                                                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                Score 1306; DB 5;
Pred. No. 2.3e-116;
8; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer associated phosphatase; enzyme; human; cancer; tumour; cyimmunosuppressive; antidiabetic; neuroprotective; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2004
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autoimmune disease. New nucleic acids encoding cancer associated phosphatases, usergets for screening pharmaceutical agents that inhibit the or for diagnosing and treating cancer, inflammation useful as ę O.

Claim 1; SEQ ID NO 10; 63pp; English

CC The present invention describes an isolated cancer associated phosphatase CC nucleic acid. Also described: (1) a method of screening for biologically CC active agents that modulate a cancer associated phosphatase function; (2) CC a method for the diagnosis of cancer; (3) a method for inhibiting the CC growth of a cancer cell; (4) methods of screening for targets of a cancer CC associated phosphatase, where the targets are associated with signal CC tumour; (6) a composition for the treatment of a tumour; (6) a composition for the treatment of a tumour comprising a CC pharmaceutical carrier and (C); (7) methods for treating a tumour; and CC pharmaceutical carrier and (C); (7) methods for treating a tumour; and CC phosphatase of the present invention has cytostatic, immunosuppressive, CC antipsoriatic, neuroprotective, antitheumatic, antiarthritic, neuroprotective, antitheumatic, antiarthritic, considered continuous in patients or diagnosing and treating cancer, e.g. CC phosphatases and nucleic acids encoding the proteins are useful for CC usualising tumours in patients or diagnosing and treating cancer, e.g. concleic acids may also be used for treating hyperproliferative diseases, condometriosis or angiogenesis, determining the effectiveness of drugs, condometriosis or angiogenesis, determining the effectiveness of drugs, condometriosis or angiogenesis, or as targets for screening pharmaceutical

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11-DEC-2001; 2001US-0339433P.
14-MAR-2002; 2002US-0365091P.
14-MAR-2002; 2002US-0365384P.
12-APR-2002; 2002US-0372381P.
12-APR-2002; 2002US-0372381P.
12-APR-2002; 2002US-03726045P.
22-APR-2002; 2002US-0376045P.
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48; Mismatches 75;
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Best Local :
                                                                                                                                                                                                       The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence was used in the exemplification of the invention.
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Ma Y,
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Wang D, Chen
                                                                                     I FGNKMNSENVKPSHHLSFSDKYELVYPEPLESDTDETVWDVSDRSLRNRWNSMDSETAG
PSQALSPLLS-----DTRKIVSEGELDQLAQIRPLIENFHEQTAIKDCLKILEEKTAA
                          PSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQKK-EE
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QTKEQYHFCYDIVLEVLRKLLTL
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                                            VNCGEEYFYIATQGPLLSTIDDFWQMVLENNSNVIAMITREMEGGIIKCYHYWPISLKKP
                                                                                                                                                                                     YDIMQEFMALELKNLPGEFYSGNQPSNREKNRYRDILPYDSTRVPLGKSKDYINASYIRI
                                                                                         LELKHERVFLENYQILQYFIIRMFQVVEKSTGTSHSVKQLQFTKWPDHGTPASADSFIKY
408
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                                             385
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                                                                                                                 379
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                                                                                                                                                                                                           259
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RESULT 10
AAE37996
ID AAE37
XX AAE37
AC AAE37
XX 06-N0
DT 06-N0
DB Human
XX Human
XX Human
XX PBOY1
KW 1chal
KW renal
KW neuro
KW acquoi
KW acquoi
KW acquoi

Human kinase and

phosphatase

(KPP-41)

protein.

AAE37996; AAE37996; 06-NOV-2003

(first

entry)

standard;

protein;

412

Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis; atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer; psoriasis; thromobocytopaemia; developmental disorder; Reiter's syndrome; renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease; neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis; autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome; acquired immune deficiency syndrome; immunosuppressive; Crohn's disease; acquired immunosuppressive; Crohn's disease; nootropic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus;

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The invention relates to an isolated polypeptide, which is a human kinase CC and phosphatase (RPP). KPP agonists and antagonists are useful for CC diagnosing, treating or preventing disorders associated with aberrant CC expression of KPP, particularly cell proliferative disorders (e.g. CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal concturnal haemoglobinuria, polycythaemia vera, psociasis, primary CC thromobocytopaenia or cancer), developmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alabemer's disease Parkinson's disease or epilepsy), autoimmune/CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, CC gout, Grave's disease, Josephrickis, osteophritis, osteophritis, riritable bowel syndrome, CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral, CC bacterial, fungal, parasitic, procozoan or helminthic infections. The KPP CC is useful in assessing the effects of exogenous compounds on the CC expression of nucleic acids and knases and phosphatases. KPP gene is useful in gene therapy and for creating transgenic animals to model human CC disease. The present sequence is human KPP protein
                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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19-DEC-2001; 2001US-0343007P.
21-DEC-2001; 2001US-0343546P.
04-FEB-2002; 2002US-0354368P.
15-FEB-2002; 2002US-0357675P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baughn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kable AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                       121
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                                                                                                                                                                       51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a AJA, buca a K, 1 MR, Chawla NK, Chawla NK, Spr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MR,
Lee
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                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                 DVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFN
                                                                                                                                                                                                                                                                                    MSSPRKVRGKTGRDNDEEEGNSGNLNLRNSLPSSSQKMTPTKPVQNKNLMKYEEHLDILM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412
                                                                                                                                                                    VELLIKTIWYNVFKLWKGKLIFGNKWNSENVKPSHHLSFSDKYELVYPEPLESDTDETVW
                                                                                                                                                                                                                               MSSPRDFRAEPVNDYEGNDSEAEDLNFRETLPSSSQENTPRSKV----------
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A, Emerling EM, Ramkumar J, Jin P,
Chawla NK, Lehr-Mason PM, Khare R,
Lee SY, Sprague WW, Zebarjadian Y;
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,
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                                                                                                                                                                                                                                                                                                                                               53.5%; Score 1304.5; DB 6; 58.6%; Pred. No. 3.3e-116; tive 50; Mismatches 89;
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-DTRKIVSEGELDQLAQIRPLIFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gorvad AE;
, Griffin
                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                          412;
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New human kinases and phosphatases and polynucleotides, useful diagnosing, treating or preventing autoimmune or inflammatory (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthricancer or hepatitis.

disorders

Baughn Hafalia AJA,

, ds

2003-532894/50. DB; AAD57366.

(INCY-) INCYTE GENOMICS

INC.

Chien D,

Chien D, Wilson AD, Swarnakar A, Go , Emerling BM, Ramkumar J, Jin P, Chawla NK, Lehr-Mason PM, Khare R, Lee SY, Sprague WW, Zebarjadian Y;

Gorvad Griffin Lee S,

JA, Hawkins

Marquis JP;

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RESULT 11
AAB37994
ID AAB37
AC AAB37
AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-2001; 2001US-0340235P
19-DEC-2001; 2001US-0343007P-
21-DEC-2001; 2001US-0343546P
04-FEB-2002; 2002US-0354388P-
15-FEB-2002; 2002US-0357675P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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AAG67637
ID AAG67
XX AAG67
XX AAG67
XX AAG67
XX AM6100
XX Human
XX Homo
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
   29-JUL-1999;
18-OCT-1999;
11-JAN-2000;
                                                                                                                    28-JUL-2000; 2000WO-JP005061
                                                                                                                                                                              08-FEB-2001.
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              Amino
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                                                                                                                                                                                                                                     WO200109316-A1.
                                                                                                                                                                                                                                                                                                                                                 Human; protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG67637 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQYQFCYEIVLEVLQNLLAL 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARKSHLTGPMVVHCSAGIGRTGVFLCVDVVFCAIVKNCSFNIMDIVAQMREQRSGMVQTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRKSHITGPLLVHCSAGVGRTGVPICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEEYFYIATQGPLPETIEDFWQNVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQYHFCYDIVLEVLRKLLTL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KHFRVFLENYQILQYFIIRMFQVVEKSTGTSHSVKQLQFTKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EHFSVFLETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEEYFYIATOGPLLSTIDDFWQWVLENNSNVIAMITREIEGGIIKCYHYWPISLKKPLEL
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                                                                                                                                                                                                                                                                                                                                                                                                           sequence of a human
   99JP-00248036.
99US-0159590P.
2000JP-00118776.
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                                                                                                                                                                                                                                                                                                                                                       kinase;
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75.8%;
                                                                                                                                                                                                                                                                                                                                                    protein
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Pred. No. 4.5e-94;
                                                                                                                                                                                                                                                                                                                                                    phosphatase; signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                              protein.
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RESULT 13
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AAG67458; AAG67458

standard;

protein;

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26-NOV-2001

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Amino acid

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Ishii S,
Senoo C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification describes human protein kinase/protein phosphatases. It is expected that the protein kinase/protein phosphatase gene participates in signal transduction in cells. The protein kinase/protein phosphatase polypeptides and polymucleotides are useful for developing diagnostics and treatment agents for human and animal diseases. The protein kinase/protein phosphatase polypeptides are useful as target molecules in designing novel drugs. The protein kinase/protein phosphatase polypeptides are source of probes and primers, which may be used to isolate homologous sequences. The present sequence represents a human protein, which is used in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-FEB-2000; 2000US-0183322P-02-MAY-2000; 2000UP-00183767.09-JUN-2000; 2000UP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1267 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New genes encoding proteins with protein kinase/protein phosphatase activity, useful in the diagnosis and treatment of diseases.
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1255
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                                                                                                                                                                                                                                                                                                                                                                           922
                                                                                                                                                                                                                                                                                                                                                                                                         108
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S, Sugiyama
C, Nezu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
A 1255
                             A 461
                                                                             GRTGVF1CVDVVFSAIEKNYSFDIMNIVTQMRKQRCCMIQTKEQYQFCYBIVLEVLQNLL 460
                                                                                                                                                                                                                                              OTKENRRKNRYKNIL PYDATRVPLGDEGGYINASFIKI PVGKEEFVYIACQGPLPTTVGD
                                                              GRSGTLI
                                                                                                                      RAMTLEDIQTREVRHISHLNFTAWPDHDTPSQPDDLLTFISYMRHIHRSGPIITHCSAGI
                                                                                                                                                    RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGP1LVHCSAGV
                                                                                                                                                                                                     FWOMVLENNCNVLAMITREIECGVIKCYSYWPISL-KEPLEEEHFSVFLETFHVTQYFTV
                                                                                                                                                                                                                                                                     NTLQNRDKNRYRDILÞYDSTRVÞLGKNKDYINASYIRIVNHEEBYFYIATQGÞLÞSTIED
                                                                                                                                                                                                                                                                                                           LAVLPVVKVLPSGKYTGANLKSVIRVLRVARSGIPSKELENLQELKPLDQCLI-----
                                                                                                                                                                                                                                                                                                                                            LTQLAQIRPLIFNSSARSAMRDCLNTLQ------KKEELDIIREFLELEQMTLPDDFNSG
                                                                                                                                                                                                                                                                                                                                                                                                     PEPLESDTDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDTETSVSEKE
                                                                                                                                                                                   FWQMIWEQKSTVIAMMIQEVEGEKIKCQRYWPNILGKTTMVSNRLRLALVRMQQLKGFVV
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                                                           CIDVVLGLISQDLDFDISDLVRCMRLQRHGMVQTEDQYIFCYQVILYVLTRLQ
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T, Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.2%;
38.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 640; DB
Pred. No. 1.5e-
52; Mismatches
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
.5e-51
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Otsuki
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1255 A 1255

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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JAN-2000;
17-FEB-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ota T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Page 305-315; 336pp; Japanese
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18-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New genes encoding protein kinase and protein phosphatase, useful for identifying modulators which can be used to treat human or animal lisorders associated with the expression or function of these enzymes.
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Sugiyama
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A 461
                                                            GRIGOFICVDVVFSAIEKOYSFDIMNIVTQMRKQRCGMIQIKEQYQFCYBIVLEVLQNLL
                                         GRSGTLICIDVVLGLISQDLDFDISDLVRCMRLQRHGMVQTBDQYIFCYQVILYVLTRLQ
                                                                                                                                             RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGFLLVHCSAGV
                                                                                                                                                                                                                                                                                     QTKENRRKNRYKNILPYDATRVPLGDEGGYINASFIKIPVGKEEFVYIACQGPLPTTVGD
                                                                                                                                                                                                                                                                                                                          NTLQNRDKNRYRDILPYDSTRVPLGKNKOYINASYIRIVNHEEEYFYIATQGPLPETIED
                                                                                                                         RAMTLEDIQTREVRHISHLNFTAWPDHDTPSQPDDLLTFISYMRHIHRSGPIITHCSAGI
                                                                                                                                                                                                       FWQMIWEQKSTVIAMMTQEVBGEKIKCQRYWPNILGKTTMVSNRLRLALVRMQQLKGFVV
                                                                                                                                                                                                                                            FWOMVLENNCNVIAMITREIECGVIKCYSYWPISI-KEPLEFEHFSVFLETFHVTQYFTV
                                                                                                                                                                                                                                                                                                                                                                      LAVIPVVKVIPSGKYTGANIKSVIRVIRVARSGIPSKELENIQEIKPIDQCLI-----G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQEKKTDDDEITWG-NDELPIERTNHEDSD-------KD-HSFLINDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPLESDIDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDTETSVSEKB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nezu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0159590P.
2000JP-00118776.
2000US-0183322P.
2000JP-00183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000WO-JP005060
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T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 640; DB 4;
Pred. No. 1.5e-51;
52; Mismatches 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashi K, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saito K,
C, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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T, Funaha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Funahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
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PEPLESDIDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDTETSVSEKE :: | | | | | | | : :: |

Query Match
Best Local Similarity
Matches 137; Conser

Conservative

62;

26.2**%**;

Score 639.5; Pred. No. 7.3 Mismatches

.3e-52; 128;

Indels Length

35;

Gaps

167 6 Sequence

766

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RESULT 14
ABUTO 688
ID ABUT
XX ABUT
XX ABUT
XX ABUT
XX ABUT
XX Huma
XX Clai
XX
                                           adipocyte cells, given in the specification. The proteins are identified by selecting a bait protein from a known adipocyte marker and then complex between two interacting proteins are identified by selecting a yeast 2-hybrid selection to isolate prey proteins encoded by CC members of an adipocyte cDNA library. The proteins are designated SID CC [RTM] (selected interacting domains) proteins. Also included are a coplymucleotide encoding a polypeptide in the adipocyte cells, a CC recombinant host cell expressing at least one of the interacting cells, a SID (RTM)) polypeptide comprising any of the 738 amino acid sequences given in the specification (including its fragment or variant), a SID (RTM) polypucleotide comprising any of the 738 nucleotide sequences given in the specification (including its fragment or variant), a vector comprising the SID (RTM) polynucleotide, a recombinant host cell comprising the SID (RTM) polynucleotide, a recombinant host cell comprising the specification (including its fragment or variant), a vector comprising the vector, a protein chip comprising the polypeptides and a recombinant host cell comprising the specification. CC The comprising all or part of the data, listed in the specification. CC The comprising metabolic disorders such as obesity or diabetes. CC particularly useful for identifying selected interacting domains (SID CC (prey) protein of the invention

CC (prey) protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prey; adipocyte; SID; selected interacting do: antidiabetic; protein-protein interaction; diabetes; yeast 2-hybrid assay; metabolic disorder; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 208-209; 382pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU70688;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             obesity or diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
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RESULT 15
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ID AAR711
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A CDNA library was prepd. from human glioma cell line U-343 MGa 31L or AGI518 human foreskin fibroblasts. Degenerate primers based on conserved regions of PTPs were prepd. Sense oligos were AAQB5926 and AAQB5927, and the antisense oligo was AAQB5928. Three clones defined novel PTP sequences. Two of these were named PTPL1 and GLM-2. The U-343 MGa 31L
                                                                                                                                                                                               New protein tyrosine phosphatase(s), PTPL1 and GLM-2 - used prods. for use in detection, diagnosis, screening assays or
                                                                                                                                                                                                                                                                                N-PSDB; AAQ85924.
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05-OCT-1995
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                                                                                                                                                     Page 56-68; 92pp; English.
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570. .885
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Best Local Similarity 37.8
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA library was screened with labeled probes corresp, to PTLP1. Th AG1518 human fibroblast cDNA library was also screened. The complet of PTPL1 was derived from six overlapping cDNA clones and is given AAQ85924. (Updated on 25-MAR-2003 to correct PN field.)
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QA 2454
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                                                        IGRSGTLICIDVVLGLISQDLDFDISDLVRCMRLQRHCMVQTEDQYIFCYQVILYVLTRL
                                                                         VRAMTLEDIQTREVRHISHLNETAWPDHDTPSQPDDLLTPISYMRHIHRSGPIITHCSAG
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                                                                                                                                                                                                      DEWOMVLENNCNVIAMITREIECGVIKCYSYWPISI-KEPLEFEHFSVFLETFHVTQYFT
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                                                                                                                                                                                                                                                                                                                           LTQLAQIRPLIFNSSARSAMRDCLNTLQ------KKEELDIIREFLELEQWTLPDDFNS
                                                                                                                                             VRVPQIVKKSTGKSQCVKHLQFTKWPDHGTPASADPFIKYVRYVRKSHITGPLLVHCSAG
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Search completed: June 18, 2004, 19:38:35 Job time : 62 secs

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Result
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Maximum
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Perfect score:
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Match Length DB
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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(without alignments)
1039.253 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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         US-08-596-291-3
US-09-100-804-3
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US-09-566-076-12
US-09-565-0518-4
US-09-655-6518-4
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US-08-447-533-2
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Sequence 3, Appli
Sequence 12, Appl
Sequence 12, Appli
Sequence 46, Appli
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Sequence 7, Appli
Sequence 7, Appli
Sequence 5, Appli
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Sequence 5, Appli
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## ALIGNMENTS

RESULT 1 US-08-596-291-3

Sequence 3, Patent No.

Application US/08596291

GENERAL INFORMATION:

APPLICANT: GONEZ, LEONEL JORGE

APPLICANT: SALAS, JAN

APPLICANT: CLAESSON-WELSH, LENA

APPLICANT: HELDIN, CARL-HENRIK

TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL

TITLE OF INVENTION: TYROSINE PHOSPHATASES

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: MOLF. GERENVIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIF: 00210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PATCHION DATA:
APPLICATION NUMBER: US/08/596,291
FILING DATE: 09-ANG-1996
CLASSIFICATION NUMBER: US/08/15,573
FILING DATE: 01-SEP-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/15,573
FILING DATE: 01-SEP-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 1.0461/7000
TELEPRAX: 617/720-3441
TELEPRAX: 617/720-3441
TELEPRAX: 92-1742 TELENGE:
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
LENGTH: 2465 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-596-291-3

Ouery Match
Best Local Similarity 37.8%; Pred. No. 1.6e-53;

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RESULT 2
US-09-100-804-3
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              APPLICATION NUMBER: US 08/115,573
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: L0461/7003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GONEZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: CLAESCON-WELSH, LENA
APPLICANT: CLAESCON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: EXPRESSION OF NUCLECTI
TITLE OF INVENTION: TYROSINE PHOSPHATASES
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 09-AUG-1996
                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE. PATENTIA RELEASE #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRAMTLEDIQTREVRHISHLNFTAWPDHDTPSQPDDLLTFISYMRHIHRSGPIITHCSAG
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                                                                       US-09-080-855-12
                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/080,855A CURRENT FILING DATE: 1998-05-18
EARLIER APPLICATION NUMBER: 08/805,583
EARLIER FILING DATE: 1997-02-25
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09080855A Patent No. 6083721
Query Match
Best Local Similarity
Matches 137; Conserv
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE 2465 amino acids
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                                                                                                                                                                                                                                                              APPLICANT: Aspenstrm, Pontus
APPLICANT: Hellman, Ulf
APPLICANT: Gonez, Leonal Jorge
APPLICANT: Heldin, Carl-Henrik
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
ETILE REFERENCE: L0461/7030
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Saras, Jan
APPLICANT: Franzn, Pe
                                                                                      ORGANISM: Homo sapiens
                                                                                                                          LENGTH: 2466
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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TELEFAX: 617-720-2441
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     62
 Score 639.5; DB 3
Pred. No. 1.6e-53;
52; Mismatches 128
                                 DB 3;
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; ORGANISM: Homo sapiens
US-09-566-076-12
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APPLICANT: Saras, Jan
APPLICANT: Aspenstrm, Pontus
APPLICANT: Heldman, Ulf
APPLICANT: Heldman, Ulf
APPLICANT: Gonez, Leonel Jorge
APPLICANT: Heldin, Carl-Henrik
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPLA
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPLA
CURRENT APPLICATION NUMBER: US/09/566,076
CURRENT FILING DATE:
EARLIER APPLICATION NUMBER: 09/080,855
EARLIER APPLICATION DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0

150CTWARE: FastSEQ for Windows Version 3.0
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  2273
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                                281 DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFT 339
                                                                                                                                                                                                                                                                            168 LTQLAQIRPLIFNSSARSAMRDCLNTLQ------KKEELDIIREFLELEQMTLPDDFNS 220
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DFWQMIWEQKSTVIAMMTQEVEGEKIKCQRYWPNILGKTTMVSNRLRLALVRMQQLKGFV 2332
                                                                                                              GQTKBNRRKNRYKNILPYDATRVPLGDEGGYINASFIKIPVGKEEFVYIACQGFLPTTVG 2272
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PCT-US94-09943-2
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GENERAL INFORMATION:
APPLICANT:
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                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617/720-2441
TELEX: 92-1742 BZEKIEL
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: P-38,3
REFERENCE/DOCKET NUMBER: LC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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APPLICATION NUMBER: US 01
FILING DATE: 01-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: TWOMEY, MICHAEL J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                       2159 LAVLPVVKVLPSGKYTGANLKSVIRVLRGLLDQGIPSKELENLQBLKPLDQCLI----- 2212
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  221 GNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHBEEYFYIATQGPLPETIE 280
                                                                                  168 LTQLAQIRPLIPNSSARSAMRDCLNTLQ------KKEELDIIREFLELEQMTLPDDPNS 220
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US-09-290-640-46
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CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 46, Application US/09290640 Patent No. 6204055
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APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation
FILE REFERENCE: ISPH-0351
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ORGANISM: Homo
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                                                                                                   VGRTGVFICVDVVFSAJEKNYSFDIMNIVTOMRKORCGMIQTKEQYQFCYEIVLEVLQNL 459
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CURRENT APPLICATION NUMBER: US/09/665,615B
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION UNMBER: US 09/290,640
PRIOR PILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 179
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 46
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SEQ ID NO 46
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local
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APPLICANT: Marcusson, Eric G.
APPLICANT: Myatt, Jacqueline
TITLE OP INVENTION: Antisense Modulation of Fas Mediated Signaling
FILE REPERENCE: ISPH-0502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 26.2%; Score 639.5; DB 4;
Local Similarity 37.8%; Pred. No. 1.6e-53;
hes 137; Conservative 62; Mismatches 128;
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QA 2473
                                                                   IGRSGTLICIDVVLGLISQDLDFDISDLVRCMRLQRHCMVQTEDQYIFCYQVILYVLTRL
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US-09-848-294-2

US-09-848-294-2

; Sequence 2, Application US/09848294

; Patent No. 6479640

; GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas K.

TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el

TITLE OF INVENTION: Protein Tyrosine Phosphotase Which Localizes to F

TITLE OF INVENTION: Adhesions and Uses Therefor

FILE REFERENCE: CSHL90-04FZA

; CURRENT FAPLICATION NUMBER: US/09/848,294

; CURRENT FILING DATE: 1999-01-22

; PRIOR APPLICATION NUMBER: 08/759,536

; PRIOR APPLICATION NUMBER: 08/759,536

; PRIOR APPLICATION NUMBER: 08/107,420

; PRIOR FILING DATE: 1996-12-04

; PRIOR FILING DATE: 1996-12-05

; PRIOR RILING DATE: 1995-08-16

; PRIOR FILING DATE: 1996-12-06

; PRIOR FILING DATE: 1995-08-16

Focal

RESULT

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LENGTH: 244
; TYPE: PRT
; ORGANISM: Homosapiens
US-09-848-294-7
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; TYPE: PRT
; ORGANISM: Homosapiens
US-09-848-294-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-848-294-7
                                                                                                                                                                           PRIOR APPLICATION NUMBER: 07/663,579
PRIOR PILING DATE: 1991-03-01
PRIOR APPLICATION NUMBER: 07/494,036
PRIOR FILING DATE: 1990-03-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASESEQ for Windows Versior
SEQ ID NO 7
Best Local Similarity Matches 101; Conserv
                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 20.5%;
Best Local Similarity 37.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
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PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 08/759,536
PRIOR FILING DATE: 1996-12-04
PRIOR APPLICATION NUMBER: 08/107,420
PRIOR FILING DATE: 1993-08-16
PRIOR FILING DATE: 1993-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el
TITLE OF INVENTION: Protein Tyrosine Phosphotase Which Localizes to Focal
TITLE OF INVENTION: Adhesions and Uses Therefor
FILE REFERENCE: CSHL90-04FZA
CURRENT APPLICATION NUMBER: US/09/848,294
CURRENT FILING DATE: 2001-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1991-03-01
PRIOR APPLICATION NUMBER: 07/494,036
PRIOR FILING DATE: 1990-03-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tonks, Nicholas K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381 RYVRKSHI-TGPLLVHCSAGVGRTGVFICVDVVFSAISKNYSFDIMNIVTQMRKQRCGMI 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          766 NHGGFHIQCQSEDCTIAYVSREMLVTNTQTGEEHTVTHLQYVAWPDHGIPDDSSDFLEFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 ---TLPDDFNSGNTLQNRDKNRYRDILFYDSTRVPLGKNKDYINASYI------RIVNH 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           607 SEDELNÓL--FPEAIFFMCPEGG--DTLEGSMAQLKKGLESGTVLIQFEQLYRKKFGLAI 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 SEKELTQLAQIRPLIFNSSARSAMRDCL--NTLQKKEELDIIREFLELEQM------
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  Conservative
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                     20.3%; Score 494; DB 4
41.7%; Pred. No. 1e-40;
38
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  Mismatches
                                        DB 4; Length 244;
85
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Indels
18,
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Gaps
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US-08-348-006B-5
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US-08-348-006B-5
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   Matches
              Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 5:
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APPLICANT: RODAN,
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,006B
FILING DATE:
                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032
FILING DATB: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J., MARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: RODAN, GIDEON A
APPLICANT: SCHMIDT, AZZIEL
APPLICANT: RUTLEBGE, SU JA
TITLE OF INVENTION: CDNA E
TITLE OF INVENTION: TYROSI
                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1911 amino aci
                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: J. WARK HAND
STREET: 126 E. LINCOLN AVE.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 120
CITY: RAHWAY
                                                                                                      STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                      TELEPHONE:
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ZIP: 07065-0900
 107;
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   Conservative
                                                                                                        linear
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                                                                                    protein
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                  20.1%;
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47;
Score 490.5; DB 1;
Pred. No. 6.4e-39;
17; Mismatches 91;
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                                Length 1911;
 Indels
21;
 Gaps
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207 LELEQMTLPDD-----FNSGNTLQNRDKNRYRDILPYDSTRVPLG-----KNKDYINAS

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Sequence 5, Appr.
No. 5866397
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PS-ENENT Release #1.0, V.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/800,825A

FILING DATE: 14-FEB-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: HAND, J. MARK

REGISTRATION NUMBER: 36,545

REFERENCE/DOCKET NUMBER: 18992DA

TELEBONNUMICATION INFORMATION:

TELEBONE ON TABLES

TELEBONE ON 
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APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 732-594-4720 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1911 amino aci
TYPE: amino acid
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STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                                                                                                          Local
                                                                                                           1643 MELEFKRLANSKAHTSRFISANLPCKKFKNRLVNIMPYESTRVCLQPIRGVEGSDYINAS
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256 YIRIVNHEESYFYIATQGPLPETIEDFWQMVLENNCNVIAMITRBIECGVIKCYSYWPIS 315
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Pred. No. 6.4e-39;
"" smatches 91;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-BOS/MS-DOS
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REGISTRATION NUMBER: 36,545
REFERENCE/DOCKST NUMBER: 18
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 08/8
FILING DATE: 14-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
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CORRESPONDENCE ADDRESS:
ADDRESSE: J. WARK HAND - MERCK & CO., INC.
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
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LENGTH: 1911 amino aci
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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ZIP: 07065-0900
1703 FID--GYRQQKAYIATQGPLAETTEDFWRMLWENNSTIVVMLTKLREMGREKCHQYWP-- 1758
                                                                          1643 MELEFKRLANSKAHTSRFISANLPCKKFKNRLVNIMPYESTRVCLQPIRGVEGSDYINAS
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                                   256 YIRIVNHEEEYFYIATQGPLPETIEDFWQWVLENNCWVIAMITREIECGVIKCYSYWPIS 315
                                                                                                             207 LELECWILPDD-----FNSGNILQNRDKNRYRDILPYDSTRVPLG-----KNKDYINAS
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CDNA BNCODING A NOVEL HUMAN PROTEIN
TYROSINE PHOSPHATASE
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PCT-US94-10166-5
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
APPLICATION NUMBER: PCT/US94/1016
FILING DATE: 09-SEPT-1994
                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 35403
REFERENCE/DOCKET NUMBER: 18:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
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FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSE: JOHN W. WALLEN III
ADDRESSEE: P.O. BOX 2000, 126 E. LINCOLN AVE.
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APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
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STREET: P.O.
CITY: RAHWAY
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LKEPLEFEHFSVF-LETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASAD 374
                                                   FID--GYRQQKAYIATQGPLAETTEDFWRMLMENNSTIVMLTKLREMGREKCHQYWP--
                                                                                                                                               LELEOMTLPDD-----FNSGNTLQNRDKNRYRDILFYDSTRVPLG-----KNKDYINAS 255
                                                                                  YIRIVNHBEEYFYIATOGPIPETIEDFWOMVLENNCNVIAMITREIECGVIKCYSYWPIS 315
                                                                                                                MELEFKRLANSKAHTSRFISANLPCKKFKNRLVNIMPYESTRVCLQPIRGVEGSDYINAS 1702
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40.2%; Pred. No. 6.4e-39;
ative 47; Mismatches 91;
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Patent No.
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; MOLECULE TYPE:
US-08-446-345-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: COTUZZÍ, LAURA A.
REGISTACION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 28-APR-1994
ATTORNBY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/OFFILING DATE: 22-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
113 AYVSREMLVTNTQTGEEHTVTHLQYVAWPDHGIPDDSSDFLEFVNYVRSLRVDSEPVLVH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1878 LRTORPANVOTEDEYOFCYQAALEYL 1903
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                                                                                                                                                                                                                   226 NRDKWRYRDILPYDSTRVPLGKWKDYINASYI-----RIVMHEEEYFYIATQGPLPET 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         431 MRKORCGMIQTKEOYOFCYEIVLEVL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375 FFIKYVRYVRKSH----ITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQ 430
                                                                                                                                                                                                                                                          h 20.0%; Score 489; DB 2; Length 23:
Similarity 42.0%; Pred. No. 2.9e-40;
00; Conservative 37; Mismatches 83; Indels
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                                                                                                                         IEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEH--FSVFLETFHVTQ 336
                                                                                                                                                                   amino acid
                                                                                  CAQEWQVVWDQKLSLIVWLTTLTERGRTKCHQYWP---DPPDVMNHGGFHIQCQSEDCTI 112
                                           YFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI-TGPLLVH 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFIDFIGQVHKTKEQFGQDGPISVHCSAGVGRTGVFITLSIVLERMRYEGVVDIFQTVKM 1877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 amino acids
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1155 Avenue of the Americas
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Moller, Karin B.
VENTION: NOVEL PROTBIN PHOSPHOTYROSINE
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US-08-685-992-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-685-992-21
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CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/605,992
FILING DATE: 25-UUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
CFENENCE/DOCKET NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-03
TELECHONE: 781-861-6240
TELEPAX: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 20.0%; Score 487; DB 2; Length 242; Best Local Similarity 41.8%; Pred. No. 5e-40; Matches 102; Conservative 37; Mismatches 79; Indels 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/08685992
Patent No. 5912138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02173
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Plint, Andrew J.
TITLE OF INVENTION: SUBSTRAIF TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tonks, Nicholas APPLICANT: Plint, Andrew J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 242 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two Mil
CITY: Lexington
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                      392 LLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEI 451
                                                                                                                              118 SEDCTIAYVSMLVTNTQTGEEHTVTHLQYVAWPDHGIPDDSSDFLEFVNYVRSLRVDSEP
  452 VLEV 455
                                       178 VLVHCSAGIGRTGVLVTMETAMCLTERNLPIYPLDIVRKMRDORAMMVOTSSOYKFVCEA 237
                                                                                                                                                                                                                                                                                                                               225 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYI-----RIVNHEEEYFYIATQGFLFB 277
                                                                                                                                                                    335 TQYFTVRVFQ--IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI-TGP 391
                                                                                                                                                                                                                                                             278 TIEDFWOMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHV--- 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 QNILDKNRYKDYLFYDTTRVILLQGNEDYINASYVNMEIPAANLVNK----YIATQGPLPH 65
                                                                                                                                                                                                                 TCAQFWQVVWDQKLSLIVMLTTLTERGRTKCHQYWP---DPPDVMNHGG----FHIQCQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Two Militia Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BROOK, SMITH & REYNOLDS, P.C.
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Search completed: June 18, 2004, 19:41:11 Job time : 25 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
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        1378.5
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/YCT0_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                          Query
Match
            June 18, 2004, 19:40:09; Search time 49 Seconds (without alignments) 2667.576 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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2439
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Copyright (c) 1993 - 2004 Compugen Ltd.
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          463
412
357
420
420
122
122
381
1267
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US-09-095-478-3
US-09-095-478-8
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US-10-619-220-46
US-10-408-765A-1349
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Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 8, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 56, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 12, Appli
Sequence 46, Appli
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15	12	5	14	14	16	14	16	12	15	15	15	14	φ	5	10	ø	14	ø	10	9	15	14	9	12	12	12	10	12	12
-10-366-547-	-09-887-669-	-10-258-666-	5-823-	-10-176-	10-	10-245-53	10-408-	09-887-669-2	US-10-369-493-6128		US-10-366-547-42	US-10-390-501-2	US-09-788-626-22	US-10-366-547-40	US-09-800-198-44	บร-09-808-602-54	US-10-293-231-7	48-294	-198-	US-09-808-602-55	Ė	<b>S-</b> 10-293-231	-09-848-294-2	-10-072-012-8	-10-218-779-	-10-087-684-	US-09-095-478-5		US-10-087-684-93
Sequence 49, Appl	e L	e 12	e 34	e 22	e 16	O	e 28,	2	ET O	4	2	Ф 22.	22,	e 40	е 4.	Çī	መ	7	o			æ	N		Œ	æ	æ	æ	Sequence 93, Appl

# ALIGNMENTS

Sequence 2, Application US/09095478 Sequence 2, Application US/09095478 Publication No. US20030095970A1 GENERAL INFORMATION: APPLICANT: Plowman, Gregory ITILE OF INVENTION: NOVEL PROTEIN TYROSINE TITLE OF INVENTION: RELATED PRODUCTS AND TITLE OF INVENTION: METHODS NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS: ANDRESSE: Lyon & Lyon STREET: Sold West Fifth Street STATE: California COUNTRY: U.S.A. ZIP: 90071-2066 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: STORAGE COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: PASTSEQ For Windows 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/095,478 FILING DATE: CLASSIFICATION DATA: APPLICATION NUMBER: US/09/095,478 FILING DATE: CLASSIFICATION NUMBER: PRIOR APPLICATION DATA: APPLICATION NUMBER: ATTORNEY/AGENT INFORMATION: ARGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 324/115 TELEPHONE: (213) 489-1600	ESULT 1
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Sequence 1, Application US/09095478
Publication No. US2030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
ITILE OF INVENTION: NOVEL PROTEIN TYROSINE
ITILE OF INVENTION: PHOSPHATASE SUPTPOS AND
ITILE OF INVENTION: RELATED PRODUCTS AND
ITILE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE PORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-09-095-478-1
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
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RESULT 3 US-09-095-478-3

Sequence 3, Application US/09095478
Publication No. US20030095970A1
GEMERAL INFORMATION:
APPLICANT: Plowman, Gregory

APPLICANT: Plowman, Gregory
TITLE OF INVENTION: MOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPTPO5 AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25

CORRESPONDENCE

ADDRESS:

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LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (213) 489-160
TELLEFAX: (213) 955-0440
TELLEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 1
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NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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SPDIMNI YTOMRKORCGMI OTKEO Y OPCYEI Y LEVLONI LALY 463
                                                                                                                                                                                        TRVPLGKNKDYINASYIRIVNHEESYFYIATQGPLPETIBDFWQWVLENNCNVIAMITRE
                                                                                 FTKWEDHGTEASADEFIKYVRYVRKSHITGELLVHCSAGVGRTGVFICVDVVFSAIEKNY 420
                                                                                                                                               IECGVIKCYSYWPISLKBPLBPEHFSVFLETFHVTQYFTVRVPQIVKKSTGKSQCVKHLQ
                                                                                                                                                                                                          TRVPLGKNKDYINASYIRIVNHEESYFYIATQGPLPETIEDFWQWVLENNCNVIAMITRE
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                                                                FTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGVFICVDVVFSAIBKNY
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Pred. No. 1.2e-194;
0; Mismatches 0; I
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COUNTRY: ....
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: TRM P.C. DC

1.44 Mb

ADDRESSEE: Lyon & Ly STREET: 633 West Fi STREET: Suite 4700 CITY: Los Angeles STATE: California

Lyon & Lyon 3 West Fifth

Street

SOFTWARE: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/095.47% FILING DATE.

COMPUTER: IBM Com OPERATING SYSTEM:

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361 FTXWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNY 420
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91.6%; Pred. No. 9.6e-185;
tive 0; Mismatches 0;
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; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: MOVEL PROTEIN
; TITLE OF INVENTION: PLATED PRODU
; TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE:
US-09-095-478-8
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US-09-095-478-8
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Best Local :
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DAT
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 81.9%; Score 1997; DB 10; Similarity 100.0%; Pred. No. 6.6e-175; 79; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                  EHFSVFLETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRY
                                                                                                                  BESYFYIATQGPLPETIEDFWQWVLENNCNVIAMITREIBCGVIKCYSYWPISLKEPLEF
                                                                                                                                                  ESEYFYIATQGPLPETIBDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEF
                                                                                                                                                                                                                                                                                                                                                                                           KTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFNSSARSAMRDCLINTLQKKEELDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIKMNSENVKPSHHLSFSDKYELVYPEPLESDTDETVWDVSDRSLRNRWNSMDSETAGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNKMNSENVKPSHHLSFSDKYELVYPBFLESDTDETVWDVSDRSLRNRWNSMDSETAGPS
EHFSVFLETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRY
                                                                                                                                                                                                                                                                                                                                                        KTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQKKEELDI
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PHOSEHATASE SUPTPOS AND
RELATED PRODUCTS AND
METHODS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 379;
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NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPACE: (213) 955-0440
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECILE TUTE: TOTAL

FILING DATE: ATTORNEY/AGENT INFORMATION: CLASSIFICATION:
PRIOR APPLICATION NUMBER:

Query Match Best Local S Matches 405

Similarity

405

Conservative

MOLECULE TYPE:

Peptide

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SEDIMNIVIONEXQECGMIQIK 405 SFDIMNIVTOWRKORCGMIQTK 442

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US-09-095-478-6
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                                                                                                                                                                                                                                                               US-09-095-478-6
                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS: LENGTH: 354 aming Type)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09095478 Publication No. US20030095970A1
                                                                                                                                                                                             Matches
                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: Pept:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE COMPATIBLE SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FASTSEQ for Windows 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095.478 FILING DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL BY
TITLE OF INVENTION: PHOSPHA:
TITLE OF INVENTION: RELATED
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: Californía
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
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                    228
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                                                                                                                                                                                           354;
                                                     £
DKNRYRDILFYDSTRVFIGKNKDYINASYIRIVNHEEEYFYIATQGFLFETIEDFWQMVL 287
                                                                      LTQLAQIRFLIFNSSARSAMRDCLNTLQXXGELDIIREFLELEQMTLPDDFNSGNTLQNR 227
                                                                                                                                         PEPLESDTDETVMDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDTETSVSEKE 167
                                                                                                                        PEPLESDIDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDTETSVSEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQYOFCYETVLEVIQUELA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQYOFCYETYLEVLONELA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRXSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRKSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTOMRKORCGMIQTK 442
                                                   LTQLAQIRPLIFNSSARSAMRDCLNTLQKKEELDIIREFLELEQMTLPDDFNSGNTLQNR
                                                                                                                                                                                                                                                                                                                                             354 amino acids
                                                                                                                                                                                     76.3%; Score 1862; DB 10; ilarity 100.0%; Pred. No. 1.6e-162; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                               ss: single
linear
                                                                                                                                                                                                                                                                              Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RELATED PRODUCTS AND
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                                                                                                                                                                                           Indels
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PRIOR APPLICATION NUMBER: PCT/US01/19442
PRIOR FILING DATE: 2001-06-14
PRIOR PLILING DATE: 2001-06-14
PRIOR PLILING DATE: 2001-06-14
PRIOR PLILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/212,447
PRIOR PLILING DATE: 2000-06-22
PRIOR PPLICATION NUMBER: US 60/215,210
PRIOR PPLICATION NUMBER: US 60/215,210
PRIOR PILING DATE: 2000-06-29
PRIOR PILING DATE: 2000-07-09
PRIOR APPLICATION NUMBER: US 60/216,529
PRIOR APPLICATION NUMBER: US 60/218,080
PRIOR APPLICATION NUMBER: US 60/218,080
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-11
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 18
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US-10-311-764-4
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                                                                                                                                                                                                                                                                                      US-10-311-764-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PERL Program
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10311764
Publication No. US20040023245A1
                                                                                                                                                                                         Matches
                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PROTEIN PHOSPHATASES FILE REFERENCE: PI-0126 USN
                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040023245A1 7476861CD1
                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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<u>4</u>5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T: BAUGHN, Mariah R.; DING, Li
T: ELIOTT, Vicki S.; GANDHI, Ameena R.
T: GRIPFIN, Jennifer A.; HAFRLIA, April J.A.
T: KEARNEY, Liam; LEE, Ernestine A.
T: LU, Yan; NGUYEN, Danniel B.
T: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
T: REDDY, Roopa M.; SANJANWALA, Madhusudan M.
T: STEMART, Elizabeth A.; TANG, Y. TOM
T: THORNTON, Michael B.; TANG, Catherine M.
T: CHAMLA, Narinder K.; YANG, Junming
T: YAO, Monique G.; YUE, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                               420
                                                                                                                                      1 MSSPRKVRGKTGRDNDEBEGNSGNLNLRNSLPSSSQXMTPTKPVQNKNLMKYEEHLDILM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CVDVVESAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYBIVLEVLQNLLA 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKNRYRDILPYDSTRYPLGKNKDYINASYIRIVNHEBEYFYIATQGPLPETIEDFWQMVL
                                        VPLLIKTIWYNVFKLWKGKLIFGNKWNSENVKPSHHLSFSDKYELVYPEPLESDTDETVW
                                                                                      MSSPRDFRAEPVNDYEGNDSEAEDLNFRETLPSSSQENTFRSKV----
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                                                                                                                                                                                         Conservative
                                                                                                                                                                                                             59.2%;
                                                                                                                                                                                         52;
                                                                                                                                                                                                             Score 1378.5; DB 16; Length 420; Pred. No. 6.1e-118;
PENKVNSEKVKLSLRNFPHNDYEDVFEEPSBSGSDPSMW
                                                                                                                                                                                         Mismatches
                                                                                                                                                                                         45,
                                                                                                                                                                                      Gaps
83
                                                120
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US-09-095-478-4
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Publication No. US20030095970A1
GENERAL INFORMATION:
                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                      INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Suite 4/0.
STREET: Suite 4/0.
CITY: LOS Angeles
CHATE: California
U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
          TOPOLOGY: linear MOLECULE TYPE: Pep:
                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: storage
CCMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FABSUSED for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                   TELEPHONE:
                                                                STRANDEDNESS:
                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 YSFDIMNIVTOMRKORCGMIQTKEQYOFCYEIVLEVLONILAL 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 QFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 STRVPLGKSKDYINASYIRIVNCGEEYFYIATQGPLLSTIDDFWQMVLENNSNVIAMITR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 SSARSAMRDCINTLOKK-EELDIIREPLELEOMTLPDDFNSGNTLONRDKNRYRDILPYD 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 BIEGGIIKCYHYWPISLKKPLELKHFRVFLENYQILQYFIIRMFQVVEKSTGTSHSVKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 EIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQIVKKSTGKSQCVKHL
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                                                                                                    122 amino acids
                                                                                                                                                                                   (213) 955-0440
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                               Peptide
                                                                single
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NOVEL TYROSINE
PHOSPHATASE SUPTPD5 AND
RELATED PRODUCTS AND
METHODS
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                                                              Matches
108 PEPL------ESDIDETVWDVS------DRSLRNRWNSMD-SETAGPSKTVSPVLSGS 152
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; MOLECULE TYPE:
US-09-095-478-7
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                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09095478 Publication No. US20030095970A1 GENERAL INFORMATION:
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                                                                                                                                                               TELEPHONE: (213) 489-16(
TELEPAX: (211) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 35.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FASTEM: IBM P.C. DOS 5.0 SOFTWARE: FASTESEQ for Windows 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095 470 FILING DATE:
                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPTPOS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 633 West Fifth
STREET: Suite 4700
CITY: Los Angara
                                                                                                  LENGTH: 381 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Californ COUNTRY: U.S.A.
     151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRXSHITGFLLYHCSAGV
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California
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     Conservative
                                                                                            یں: single
linear
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                                                                                    Peptide
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26.4%; Score 644.5; DB 10; 38.4%; Pred. No. 1.8e-50; tive 66; Mismatches 125;
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 Indels 51;
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; LENGTH: 1267
; TYPE: PRT
; ORGANISM: Homo s
US-10-060-065-35
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US-10-060-065-35
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    Query Match
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Publication No. US20030017480A1
                                                                                                                  SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jun-Ichi Nezu
APPLICANT: Jun-Ichi Nezu
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-099002
CURRENT APPLICATION NUMBER: US/10/060,065
CURRENT FILING DATE: 2002-01-29
CURRENT FILING DATE: 2002-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                   PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/JP00/05061 PRIOR FILING DATE: 2000-07-28
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                                                                                                                                                                                                                            PILING DATE: 2000-01-11
APPLICATION NUMBER: JP 2000-183767
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/159,590
FILING DATE: 1999-10-18
APPLICATION NUMBER: US 60/183,322
FILING DATE: 2000-02-17
                                                                                                                                                                                                              FILING DATE: 2000-05-02
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 2000-118776
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 11-248036 FILING DATE: 1999-07-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NASYIRIVNHEEEYFYIATQGPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYW
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Shizuko Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetsuo Nishikawa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shin-Ichi Funahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetsuji Otsuki
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    Score
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    640;
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Length
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RESULT 10
US-10-059-585-56
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                                                                                                                                    FILE REFERENCE: 06501-098001

CURRENT APPLICATION NUMBER: US/10/059,585

CURRENT FILING DATE: 2002-01-29

PRIOR APPLICATION NUMBER: PCT/JP00/05060

PRIOR FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: US 60/183,322

PRIOR FILING DATE: 2000-02-17

PRIOR PILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: US 60/159,590

PRIOR PILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: JP 2000-118776

PRIOR APPLICATION NUMBER: JP 2000-183767

PRIOR APPLICATION NUMBER: JP 2000-183767
SOFTWARE: FastSEQ
SEQ ID NO 56
LENGTH: 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 56, Application US/10059585
Publication No. US20030082776A1
GENERAL INFORMATION:
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APPLICANT:
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                                                                         PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 11-248036
PRIOR FILING DATE: 1999-07-29
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Senoo, Chiaki
APPLICANT: Nezu, Jun-Ichi
TITLE OP INVENTION: NOVEL GENES ENCODING PROTEIN
TITLE OP INVENTION: KINASE/PROTEIN PHOSPHATASE
                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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Wakamatsu, Ai
Nagai, Keiichi
Otsuki, Tetsuji
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Ishii, Shizuko
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Otsuka, Kaoru
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Nishikawa, Te
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                                         for Windows Version 4.0
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2: Mismatches 128;
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RESULT 11
US-09-095-478-9
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US-10-059-585-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
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ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS
SOFTWARE: FASTSEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,
FILING DATE:
                                                                                                                                                                                                                                                                    ZIE: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                           STREET: 633 West Fi
STREET: Suite 4700
CITY: Los Angeles
                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 90071-2066
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                                                                                                                                                                                                                                                                                                                                                                California
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633 West Fifth Street
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NOVEL PROTEIN TYROSINE
PHOSPHATASE SUPTPOS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RELATED PRODUCTS AND METHODS
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                   224/115
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Aspenstrm, Petra

Aspenstrm, Pontus

APPLICANT: Hellman, UIf

Gones, Leonel Jorge

APPLICANT: Heldin, Carl-Henrik

ITILE OF INVENTION: PAGE, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1

FILE REFERENCE: L046/1/030

CURRENT PILING DATE: 2002-06-21

FRIOR APPLICATION NUMBER: US/10/177,980

CURRENT PILING DATE: 1998-05-18

FRIOR FILING DATE: 1998-05-18

FRIOR FILING DATE: 1998-05-18

FRIOR FILING DATE: 1993-00-25

SOFTWARE: PastSEQ for Windows Version 3.0

SEQ ID NO 12

LENGTH: 2466

TYPE: PAT

ORGANISM: HOT-
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TELEPAX: (213) 955-0440
TELEPAX: 67-3510
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 26.2%;
Best Local Similarity 37.8%;
Matches 137; Conservative 6
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Pred. No. 4.7e-50;
32; Mismatches 128; Indels 35;
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US-09-802-669-46
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j ORGANISM: Homo sapiens
US-09-802-669-46
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Patent No. US20020004490A1
                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 46
LENGTH: 2485
                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhang, Hong
TITLE OF INVENTION: Antisense Compound Modulation
FILE REFERENCE: 159H-545
CURRENT APPLICATION NUMBER: US/09/802,669
CURRENT FILING DATE: 2001-03-09
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/665,615
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/290,640
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Marcusson, Eric G.
APPLICANT: Wyart, Jacqueline
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                                                GNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIB 280
                                                                                           LAVLPVVKVLPSGKYTGANLKSVIRVLRGLLDQGIPSKELENLQELKPLDQCLI-----
                                                                                                                                 LTQLAQIRPLIFNSSARSAMRDCLNTLQ-----KKEELDIIREFLELEQMTLPDDFNS
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CURRENT PILING DATE: 2003-07-14
PRIOR APPLICATION NUMBER: 09/802,669
PRIOR PILING DATE: 2001-03-01
PRIOR PILING DATE: 2001-03-01
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR FILING DATE: 1999-04-12
PRIOR FILING DATE: 1999-04-12
VUMBER: 05 SEQ ID NO 46
LENGTH: 2485
TYPER: PET
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US-10-619-220-46
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Best Local :
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TYPE: PRT
ORGANISM: Homo:
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APPLICANT: Myart, Jacqueline
APPLICANT: Zhang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
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                                                          VGRTGVFICVDVVFSAIEKVYSFDIMNIVTOMRKORCGMIQTKBQVQFCYEIVLEVLQNI
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                                                                                                         VRAMTLEDIQTREVRHISHLMFTAWEDHDTPSQPDDLLTFISYMRHIHRSGPIITHCSAG
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                                         IGRSGTLICIDVVLGLISQDLDFDISDLVRCMRLQRHGMVQTEDQYIFCYQVILYVLTRL
                                                                                                                                                VRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAG
                                                                                                                                                                                     DFWQMIWEQKSTVIAMMTQEVEGEKIKCQRYWPNILGKTTMVSNRLRLALVRMQQLKGFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.2%; Score 639.5; DB 1 37.8%; Pred. No. 8.1e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12;
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459

2411

**9**99

2351

2291

2231 220 2177 167

339

2471

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APPLICANT: Ghosh, Soumitra S.
APPLICANT: ABDY, Boin D.
APPLICANT: Schang, Bing
APPLICANT: Glbson, Bradford W.
APPLICANT: Glbson, Bradford W.
APPLICANT: Harnork, Daie S.
APPLICANT: Harnork, Daie S.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOPTWARE: FASSEQ for Windows Version 4.0
SEQ ID NO 1349
LENGTH: 2485
TYPE: PRT
ORGANISM: Homo sapiens
Search completed: June 18, 2004, 19:46:03 Job time : 50 secs
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US-10-408-765A-1349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 26.2%; Score 639.5; DB 16; Length 2485; Best Local Similarity 37.8%; Pred. No. 8.1e-49; Matches 137; Conservative 62; Mismatches 128; Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1349, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION:
                                                                                        2472 QA 2473
                                                                                                                                                                                2139 POEKKTDDDEITWG-NDELPIERTNHEDSD------KD-HSFLTNDE 2177
                                                                                                                                                                                                                                                                          2352 VRAMTLEDIQTREVRHISHINFTAWPDHDTPSQPDDLLTFISYMRHIHRSGPIITHCSAG 2411
                                                                                                                                                                                                                                                                                                                                                                2292 DEWOMIWEOKSTVIAMMTOEVEGEKIKCORYMPNILGKTTMVSNRLRLALVRMOQLKGFV 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2232 GOTKENRRKNRYKNILPYDATRVPLGDEGGYINASFIKIPVGKEEFVYIACQGPLPTTVG 2291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2178 LAVLPVVKVLPSGKYTGANLKSVIRVLRGLLDQGIPSKELENLQELKPLDQCLI----- 2231
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                                                                                                                                         460 LA 461
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                                                                                                                                                                                                                                                                                                                                                                                                            281 DFWQMVLENNCNYLAMITREIECGVIKCYSYWPISI-KEPLEFEHFSVFLETFHVTQYFT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 GNTLQNRDKNRYRDILÞYDSTRVÞLGKNKDYINASYIRIVNHEEEFFYJATQGÞLÞETIE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 LTOLAQIRELIENSSARSAMEDCLNTLQ------KKEELDIIREFLELEQMTLPDDFNS 220
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Result
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Maximum :
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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   on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB seq length: 0
DB seq length: 2000000000
                  488.5
487.487.487.484.487.484.483.484.5
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1: pir1:*
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Match
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2439
1 MSSPRKVRGKTGRDNDEEEG.....QYQFCYEIVLEVLQNLLALY 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             June 18, 2004, 19:36:23 ; Search time 20 Seconds (without alignments) 226.834 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283366 segs, 96191526 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
 GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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 158345
A48066
B48758
A488758
I58148
I546217
A53978
S68700
S50893
S12050
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A57068
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A56178
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A41105
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468. 5 19.2 1290 2 A56493 leucocyte common 468 19.2 1452 1 1517669 protein-tyrosine-p 468 19.2 1691 1 D54689 protein-tyrosine-p 468 19.2 1894 2 C54689 protein-tyrosine-p 467.5 19.2 387 1 A60345 protein-tyrosine-p 467.5 19.2 1897 1 TDHULK protein-tyrosine-p 467.5 19.1 2314 1 A46151 protein-tyrosine-p 466.5 19.1 415 1 A33899 protein-tyrosine-p 466.5 19.1 1898 2 S46216 protein-tyrosine-p 466 19.1 1452 1 S17670 protein-tyrosine-p 463 19.0 405 2 149372 protein-tyrosine-p 463 19.0 405 2 149372 protein-tyrosine-p 463 18.9 1188 1 A57064 protein-tyrosine-p 5 1188 1 1452 1 S66613 protein-tyrosine-p 5 1216 2 S66613	45	44	43	42	41	40	9	85	37	36	35	34	E	32	31	30
1290 2 A56493 1452 1 S17669 1691 1 D54689 1894 2 C54689 1897 1 TDHULK 2314 1 A46151 415 1 A33899 1898 2 S46513 1440 2 J63613 1440 2 J63613 1440 2 J63613 1440 2 J63613	461	461.5	462	462	463	466	466	466.5	466.5	467	467.5	467.5	468	468	468	468.5
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	382	1440	1216	1188	405	1452	377	1898	415	2314	1897	387	1894	1691	1452	1290
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leucocyte protein-t protein-t protein-t protein-t protein-t leukocyte protein-t leukocyte protein-t protein-t protein-t protein-t protein-t protein-t protein-t protein-t	A38191	JC6312	860613	A57064	149372	S17670	A48711	S46216	A33899	A46151	TUHULK	A60345	C54689	D54689	S17669	A56493
	protein-tyrosine-p	protein-t	protein-t	protein-t	protein-t	protein-t	protein-t	leukocyte	protein-t	protein-t	leukocyte antigen-	protein-t	protein-tyrosine-p	protein-t	protein-tyrosine-p	leucocyte common

# ALIGNMENTS

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ర్ట	Ş	дb	Q	뮹	Ş	В	Ş	Дb	Ş	Db	Ą	망	Ş	Query M Best Lo Matches	A;Note: C;Super F;161-3	A; Experimen C; Genetics:	A; Cros		A;Reference A:Accession	submitted	C; Accession: R: Ansorge. W	C;Date:	protein-ty	RESULT
375 QTKBQYHFCYDIVLEVLRKLITL 397	440 QTKEQYQFCYEIVLEVLQNLLAL 462	315 IRYARKSHLTGPMVVHCSAGIGRTGVFLCVDVVFCAIVKDCSFNIMDIVAQMREQRSGMV 374	TGPLLVHCSAGVGRTGVFICVDVVPSAIEKNYSF	255 LELKHFRVFLENYQILQYFIIRMFQVVEKSTGTSHSVKQLQFTKWPDHGTFASADSFIKY 314	320 LEPEHFSVPLETPKVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKMPDHGTPASADFFIKY 379	195 VNCGEEYFYIATQGPLLSTIDDFWQMVLENNSNVIAMITREMEGGIIKCYHYWPISLKKP 254	-BC	135 YDIMQEFMALELKNIPGEFYSGNQPSNREKNRYRDILPYDSTRVPLGKSKDYINASYIRI 194	KNRYRDILPYDSTRVPLGK	82 PSQALSPLLSDTRKIVSEGELDQLAQIRPLIFNFHEQTAIKDCLKILEEKTAA 134	TVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFNSSA	22 VPENKVNSEKVKISIRNPPHNDYEDVPEEPSESGSDPSMWTARGPFRRDRWSSEDEEAAG 81	81 IFGNKMASENVKPSHHLSFSDKYELVYPEPLESDTDETVMDVSDRSLRNRMNSMDSETAG 140	y Match 53.5%; Score 1306; DB 2; Length 398; Local Similarity 65.8%; Pred. No. 2.4e-86; hes 252; Conservative 48; Mismatches 75; Indels 8; Gaps 2;	A;Note: DKFZp566K0524.1 C;Superfamily: protein-tyrosine-phosphatase homology F;161-379/Domain: protein-tyrosine-phosphatase homology <ptp></ptp>	tal source	Cross-references: EMBL:AL050040	type: 1	number: Z16472 : T08716	to the Protein Sequence D	W.: Wirkner, U.: Mewes, H.W.: Gassenhiber, J.: Wieman	un-1999 #seq	protein-tyrosine-phosphatase homolog DKFZp566K0524.1 - human (fragment) C:Species: Homo sapiens (man)	1

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A;Map position: 5

A;Map position: 5

C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
C;Superfamily: protein 4.1 membrane-binding domain homology class; transmembrane protein; tyros
F;566-860/Domain: protein 4.1 membrane-binding domain homology <B41>
F;1089-1165/Domain: GLGF domain homology <GLG2>
F;1089-1167/Domain: GLGF domain homology <GLG2>
F;1437/Domain: GLGF domain homology <GLG3>
F;1769-1840/Domain: GLGF domain homology <GLG3>
F;1769-1840/Domain: GLGF domain homology <GLG5>
F;2003-2422/Domain: GLGF domain homology <GLG5>
F;2303-2422/Domain: GLGF domain homology <GLG5>
F;2303-2422/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;2303-2422/Domain: gubsphocysteine intermediate) #status predicted
F;2380/Binding site: substrate phosphate (Arg) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA, R;Residues: 1338-1354, K;,1356-1447, 'R',1449-1454 <RE2>
A;Residues: 1338-1354, K;,1356-1447, 'R',1449-1454 <RE2>
A;Cross-references: GB:L34581; NID:g806295; PIDN:AAC42055.1; PID:g806296
R;Hendriks, W; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submitted to the EMBL Data Library, June 1993
A;Description: Assessment of the expression levels of murine protein-tyronal contents.
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R;Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.
Science 268, 411-415, 1995
A;Title: FAP-1: a protein tyrosine phosphatase that associates with A;Reference number: I59595; MUID:95232528; PMID:7536343
A;Accession: I81210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 13 - mouse N;Alternate names: epidermal growth factor-binding protein; serine proteinas C;Species: Mus musculus (house mouse)
C;Date: 27-Nov-1997 #Bequence revision 12-Dec-1997 #text_change 21-Jun-2002 C;Accession: S71625; S67987; T81210; I81209; S40290
R;Chida, D.; Kume, T.; Mukouyama, Y.; Tabata, S.; Nomura, N.; Thomas, M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1329-1354, K',1356-1447, 'R',1449-1454 <RES>
A;Cross-references: GB:L34582; NID:g806297; PIDN:AAC42056.1;
A;Accession: IB1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Wolf, B.B.; Brown, M.D.
FEBS Lett. 376, 177-180, 1995
A;Title: Epidermal growth factor-binding protein activates soluble
A;Reference number: S67987; MUID:96105375; PMID:7498536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-2450 <CHI>
A;Cross-references: EMBL:D83966; NID:g1232103;
A;Experimental source: strain DBA/2; cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEBS Lett. 358, 233-239, 1995
A;Title: Characterization of a protein tyrosine phosphatase
A;Reference number: S71625; MUID:95145716; PMID:7843407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:Z23059; NID:g438155; PIDN:CAA80594.1; PID:g438156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 2266-2372 <HEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 1098-1102 < WOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S67987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reference number: S40280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                   106 VYPEPLESDTDETVWDVSDRSLRNRWNSM---
                                                                                                                                                                                                                                            Similarity
                       PEDVPESVSSGEGKVDLASLTAASQEEKPIEEDATQESRNSTTETTDGEDSSKDPPPLTN 2141
                                                                                                                       IYDDPQEAEVIQSLLDVVDEEAQNLLNQRHATRRACSPDPLRTNGEAPEEGDTDYNGSPL
                                                                      ---DSETAGPSKTVSPVLSGSSRLSK---
                                                                                                                                                                                                                                                                                                            Cys (phosphocysteine interm
substrate phosphate (Arg)
                                                                                                                                                                                                                                            26.7%;
35.1%;
                                                                                                                                                                                                                       68
                                                                                                                                                                                                                                         Score 650; DB 2;
Pred. No. 4.9e-38;
                                                                                                                                                                                                                  Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN:BAA12158.1; PID:g1232104
MEL 745A
                                                                                                                                                                                                                                                              Length 2450;
                                                                                                                                                                                                                    Indels
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                                                VLQNLLA
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protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 30-Jun-2002 Homo sapiens (man) splice

FEBS Lett. 337, 200-206. 1004 M.; Harada, Ġ

A;Title: Molecular cloning of a novel protein-tyrosine phosphatase A;Reference number: I53483; MUID:94116679; PMID:8287977 A;Accession: I67630 containing a membrane

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2294 <RES>
A;Cross-references: GB:D21211; NID:g452193; PIDN:BAA04752.1; PID:g45;
A;Cross-references: GB:D21211; NID:g452193; PIDN:BAA04752.1; PID:g45;
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLG
C;Keywords: phosphoric monoester hydrolase
C;Keywords: phosphoric monoester hydrolase
C;Keyhords: phosp F;2046-2265/Domain: protein-tyrosine-phosphatase homology <PTP: PIDN:BAA04752.1; PID:g452194 , nonreceptor type 13; GLGF d domain homology;

108 PEPLESDTDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDTETSVSEKE Similarity Conservative 26.2%; 62: Score 639.5; DB Pred. No. 2.5e-37 Mismatches 128; Indels ŝ Gaps 167 9

DB 2;

Length 2294;

GNTLONROKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYLATOGPLPETIE LAVEPVVKVLPSGKYTGANLKSVIRVLRGLLDQGIPSKELENLQELKPLDQCLI-----LTQLAQIRPLIFNSSARSAMRDCLNTLQ-----KKEELDIIREFLELEQMTLPDDFNS POSKKTODOBITWG-NDBLPIERTNHEDSD---KD-HSFLTNDE 1986 280 2040

DFWQMYLENNCNVIAMITRBIBCGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFT 339 DFWQMIWEQKSTVIAMMTQEVEGEKIKCQRYWPNILGKTTMVSNRLRLALVRMQQLKGFV 2160 GQTKENRRKNRYKNILPYDATRVPLGDEGGYINASFIKIPVGKEEFVYIACQGPLPTTVG VRAWTLEDIQTREVRHISHLNFTAWPDHDTPSQPDDLLTFISYMRHIHRSGPIITHCSAG VRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGFLLVHCSAG 2220 399 2100

2221 IGRSGTLICIDVVLGLISQDLDFDISDLVRCMRLQRHGMVQTBDQYIFCYQVILYVLTRL vGRTGVEICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQNL 459 2280

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protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice for N.Alternate names: Pas-associated phosphatase PAP-1; protein-tyrosine-phosphatase C; Species: Homo sapiens (man) C; Date: 11-Nov-1994 #sequence revision 08-Feb-1996 #text_change 21-Jun-2002 C; Accession: A54971, A55114; T59595; I53483; S46955 R; Banville, D.; Ahmad, S.; Stocco, R.; Shen, S.H. J. Biol. Chem. 269, 22320-22327, 1994 J. Biol. Chem. 269, 22320-22327, 1994 A; Reference number: A54971; MUID:94350988; PMID:8071359 A; Accession: A54971; MUID:94350988; PMID:8071359 A; Molecule type: mRNA
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A; Residues: 1-2466 «RES»
A; Cross-references: GB:D21210; NID:9452191; PIDN:BAA04751.1; PID:9452192
C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF dd
C; Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
FEBS Lett. 337, 200-206, 1994
A;Title: Molecular cloning of a novel protein-tyrosine phosphatase
A;Reference number: I53483; MUID:94116679; PMID:8287977
A;Accession: I67629
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;574-868/Domain: protein 4.1 membrane-binding domain homology <B41>F;1354-1430/Domain: GLGF domain homology <GLG2>
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A;Cross-references: GDB:306348; OMIM:600267

A;Map position: 4q21.3-4q21.3

C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyros
F;574-868/Domain: protein 4.1 membrane-binding domain homology <GLG1>
F;1099-1175/Domain: GLGF domain homology <GLG2>
F;1373-1454/Domain: GLGF domain homology <GLG3>
F;1511-1590/Domain: GLGF domain homology <GLG3>
F;1591-1870/Domain: GLGF domain homology <GLG3>
F;1591-1870/Domain: GLGF domain homology <GLG4>
F;1893-1967/Domain: GLGF domain homology <GLG5>
F;2442-2461/Domain: GLGF domain homology <GLG5>
F;2442-2461/Domain: Drotein-tyrosine-phosphatase homology <PTP1>
F;2410/Active site: Cys (phosphorysteine intermediate) #status predicted
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A;Residues: 1-61.'GS',64-839,'D',841-1210,'I',1212-1383,1389-2299,'QM',2302-2490
A;Cross-references: GB:D21209; NID:g452189; PIDN:BAA04750.1; PID:g452190
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A;Title: Molecular cloning of a novel protein-tyrosine phosph A;Reference number: I53483; MUID:94116679; PMID:8287977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Sato, T.; Irie, S.; Kitada, S.; Reed, J.C. Science 268, 411-415, 1995
Science 268, 411-415, 1995
A;Title: FRP-1: a protein tyrosine phosphatase that associates with A;Reference number: 159595; MUID:95232528; PMID:7536343
A;Accession: 159595
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A;Residues: 1-61,'GS',64-839,'D',841-1055,1075-1133,'FH',1136-1210,'I',1212-1383,1389-1
A;Cross-references: GB:X80289; NID:g515030; PIDN:CAA56563.1; PID:g515031
R:Sato. T.; Irie, S.; Kitada, S.; Reed, J.C.
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A;Cross-references: GB:U12128
A;Cross-references: SHOWN follows authors' translation at positions 62-63
A;Note: sequence shown follows authors' translation at positions 62-63
R;Saras, J.; Claesson-Welsh, L.; Heldin, C.H.; Gonez, L.J.
J. Biol. Chem. 269, 24082-24089, 1994
A;Title: Cloning and characterization of PTFL1, a protein tyrosine phosphatase
A;Reference number: A55114; MUID:95014139; PMID:7929060
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A; Residues: 1279-1888 < RES>
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                                                            VGRIGVEICVDVVFSAIEKNYSEDIMNIVIOMRKORCGMIQTKEQYOFCYEIVLEVLQNL
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IGRSGTLICIDVVLGLISQDLDFDISDLVRCMRLQRHGMVQTEDQYIFCYQVILYVLTRL
                                                                                                                                       VRAMTLEDIQTREVRHISHLNFTAWPDHDTPSQPDDLLTFISYMRHIHRSGPIITHCSAG
                                                                                                                                                                                                   VRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAG 399
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37.3%; Pred. No. 1.16
Live 64; Mismatches
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A;Map position: 1q32.2-1q32.2
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-l C;Superfamily: protein-tyrosine-phosphatase; cykeywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase; F;33-302/Domain: protein 4.1 membrane-binding domain homology <B41>
F;53-302/Domain: protein 4.1 membrane-binding domain homology <B41>
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A; Residues: 1-1187 < SMI>
A; Cross references: EMBL: X82676;
A; Experimental source: breast
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A;Title: PEZ:a novel human cDNA encoding protein tyrosine phosphatase-and ezrin-like A;Reference number: JC4155; MUID:95251727; PMID:7733990
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C;Date: 27-Aug-1995 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000 C;Accession: JC4155
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F;709-716/Region: acidic
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C;Accession: JC2366
R;Sawada, M.; Ogata, M.; Fujino, Y.; Hamaoka, T.
R;Sawada in Siophys. Res. Commun. 203, 479-484, 1994
A;Title: cDNA cloning of a novel protein tyrosine
                                                                                                                                              protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - mouse N;Alternate names: PEZ protein; protein-tyrosine-phosphatase PTP36; protein C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 24-Feb-1995 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000 C;Date: 24-Feb-1995 #text_change 21-Jul-2000 C;Date: 24-Feb-1995 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000 C;Date: 24-Feb-1995 #text_change 21-Jul-2000 C;Date: 24-Feb-1996 #text_change 21-Jul-2000 C;Date: 24-Feb-1995 #text_change 21-Jul-2000 C;Date: 24-Feb-1996 #text_change 21-Jul-2000 C;Date: 24
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F;842/Active site: Cys (phosphocysteine intermediate) #status predicted
F;848/Binding site: substrate phosphate (Arg) #status predicted
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G;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; |
G;Keywords: phosphoprotein, phosphoric monoester hydrolase; tyrosine-specific phosphata:
F;31-308/Domain: protein 4.1 membrane-binding domain homology <B41>
F;516-590/Domain: GLGF domain homology <GLG>
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Proc. Natl. Acad. Sci. U.S.A. 88, 5949-5953, 1991
A;Title: Isolation of a cDNA clone encoding a hum
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N;Alternate names: PTPH1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EH--FSVFLETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----YIATQGPLPHTCAQFWQVVWDQKLSLIVMLTTLTERGRTKCHQYWP----DPPDVM
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37.4%; Pred. No. 6e-28;
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protein tyrosine

phosphatase with

homology

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cytoskele

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C;Accession: T30938
R;Gershon, T.R.; Baker, M.; Nitabach, M.; Wu, P.; Macagno, submitted to the EMBL Data Library, December 1997
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                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-2051 <GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor tyrosine phosphatase - medicinal leech
(;Species: Hirudo medicinalis (medicinal leech)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change
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F;712-718/Region: acidic
F;935-1171/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;935-1171/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1123/Active site: Cys (phosphocysteine intermediate) #status prodicted
F;1129/Binding site: substrate phosphate (Arg) #status predicted
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A;Molecule type: mRNA
A;Residues: 1-1189 <SAM>
A;Residues: 1-1189 <SAM>
A;Cross-references: GB:D31842; NID:g507330; PIDN:BAA06628.1; PID:g507331
A;Cross-references: GB:D31842; NID:g507330; PIDN:BAA06628.1; PID:g507331
A;Experimental source: thymus
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific
C;Keywords: protein 4.1 membrane-binding domain homology <B41>
F;23-302/Domain: protein 4.1 membrane-binding domain homology <B41>
                                                                                                                                                                                                                                                           A;Cross-references: BMBL;AF017083; NID:g2695654; PID:g2695655; PIDN:AAB91460.1
                                                                                                                                                                                                                                                                                                                                                                  A;Accession:
                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: Z20939
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                                                      Query Match
Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                  Superfamily: leukocyte antigen-related protein; fibronectin type
                                                                                                                                                                                                                                     Genetics:
                                                                                                                                                                                                                                                                                                                                 Status: preliminary; translated from GB/EMBL/DDBJ
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        205 EFLELEQ-MTLPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLG-----KNKDYINASYIR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 SMDSETAGPSKTVSPVLSGSSRLSKD-----TETSVSEKELT-----
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                                                           Conservative
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                                                      Score 497; DB 2;
Pred. No. 3.8e-27;
6; Mismatches 95
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                                                                                                      Length 2051;
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A;Experimental source: ovary
A;Note: sequence extracted from NCBI backbone (NCBIN:149759, NCBIP:149760)
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 9; cellular retinaldehyde
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphata
F;38-227/Domain: cellular retinaldehyde-binding protein homology <CRB>
F;318-564/Domain: protein-tyrosine-phosphatase homology <FPP>
F;516/Active site: Cys (phosphocysteine intermediate) #status predicted
F;522/Binding site: substrate phosphate (Arg) #status predicted
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A; Residues: 1-597 < DEL>
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J. Biol. Chem. 269, 19639-19645, 1994
A;Title: Characterization of two structurally related Xenopus
A;Reference number: A53978; MUID:94308257; PMID:8034733
A;Accession: B53978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type PTPX10 - Afric. C;Species: Xenopus laevis (African clawed frog)
C;Date: 25-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 22-Jun-1999
C;Accession: B53978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 NLMKYEEHLDILMVFLLIKTIWYN----VFKLW-----KGKLIFGNKMNSENVKPS--
                                                                                                 LBFEHFSVFLETFHVT--QYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFI
                                                                                                                                                                                       VNHEEEYFYIATQGPLPETIEDFWQWVLENNCNVIAMITREIECGVIKCYSYWPISLKEP
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                                                   EDTGHF---IIRNIHIDLFQDFKLTHFEVYNKQTDESRSVAHYQYMSWPDFGVPKSASAML
                                                                                                                                                    -GYKRKNAYIATQGPLPKTPDDPWRMVWEQKVLIIVMTTRVIERGRIKCGQYWPLEAGRS
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                                                                                                                                                                                                                                                                                                      EFLELEOMTLPDDENSGNTLONRDKNRYRDILPYDSTRVPLG-----KNKDYINASYIRI 259
                                                                                                                                                                                                                                                                                                                                                            LPPGMELSLHMPEDGGMMV----
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28.6%; Pred. No. 2.6e
ative 76; Mismatches
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-SHITG-PLLVHCSAGVGRTGVFICVDVVFSAIEKNYSF 422
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C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; C;Keywords: phosphorotein; phosphoric monoester hydrolase; tyrosine-specific phosphate F;31-308/Domain: protein 4.1 membrane-binding domain homology <B41>
F;523-597/Domain: GLGF domain homology <GLG-F;523-597/Domain: protein-tyrosine-phosphatase homology <PP>F;679-900/Domain: protein-tyrosine-phosphatase homology <PP>F;852/Active sites: Cys (phosphocysteine intermediate) #status predicted F;853/Binding site: substrate phosphate (Arg) #status predicted
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A;Residues: 1-926 <GUA>
A;Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Gu, M.; York, J.D.; Warshawsky, I.; Majerus, P.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 5857-5871, 1991
A;Title: Identification, cloning, and expression of a cytosolic
A;Reference number: A41105, MUID:91288564; PMID:1648233
A;Accession: A41105
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137; Conserv
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                                                                                                                                                                                                              NNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ---I
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                      GVLITMETAMCLIECNOPVYPLDIVRTMRDQRAMMIQTPSQYRFVCEAILKVYE
                                                       GVPICVDVVFSAIEKNYSFDIMNIVTQWRKQRCGMIQTKEQYQFCYEIVLEVLQ 457
                                                                                             FNQEKNESRPLTQIQYIAWPDHGVPDDSSDFLDFVCHVRNKRAGKEEPVVVHCSAGIGRT
                                                                                                                                  VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI--TGPLLVHCSAGVGRT
                                                                                                                                                                       QGSSMVVMLTTQVERGRVKCHQYWP----EPTGSSSYGCYQVTCHSEEGNTAYIFRKWTL
                                                                                                                                                                                                                                                  SPYDATRVILKGNEDYINANYINMEIPSSSIINQ----YIACQGPLPHTCTDFWQMTWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HINETFDIPSSPEKPTPNGGIPHDNLVLIRMKPDENGRFGFNVKGGYDQKMPVIVSRVAP 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74; Mismatches 173;
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line MEG-10
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F;1245/Binding
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A;Cross-references: GB:D37781; NID:g633072; PIDN:BAA07035.1; PID:g633073
C;Comment: Enhanced expression of this protein with increasing cell density suggests a C;Comment: Shanced expression of this protein with increasing cell density suggests a C;Comment: Shanced expression of this protein with increasing cell density suggests a C;Const: references: GDB:385040; CMIM:600925
A;Cross-references: GDB:385040; CMIM:6009
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A;Title: Molecular cloning, characterization, and chromosomal A;Reference number: I52599, MUID:95086212; PMID:7994032
A;Accession: I52599
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C;Date: O1-Mar-1996 #sequence_revision O8-Mar-1996 #text_change 22-Jun-1999 C;Accession: I38670; I52599
R;Ostman, A.; Yang, O.; Tonks, N.K.
Proc. Natl. Acad. Sci. U.S.A. 91, 9680-9684, 1994
A;Title: Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, A;Reference number: I38670; MUID:95024024; PMID:7937872
A;Accession: I38670; MUID:95024024; PMID:7937872
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F;972-988/Jomain: transmembrane #status predicted (TMN)>
F;1065-1287/Domain: protein-tyrosine-phosphatase homology (PTP)
F;1065-1287/JOmain: protein-tyrosine-phosphatase homology (PTP)
F;72,82,93,104,142,172,192,231,258,278,342,351,376,391,396,413,431,501,525,536,582,603,4
F;72,82,93,104,142,172,192,231,258,278,342,351,376,391,396,413,431,501,525,536,582,603,4
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A;Residues: 1-216,'ITGVRKAA',225-260,'G',262-285,'GTEGGLDASNTERSRA',302,'S',304,'TAPVHD:
A;Cross-references: GB:D37781; NID:g633072; PINN:BAA07035.1; PID:g633073
C;Comment: Enhanced expression of this protein with increasing cell density suggests a
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A;Cross-references: EMBL:U10886; NID:g558754; PID:g558755
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KQSPPESPILVHCSAGVGRTGTFIAIDRLIYQIENENTVDVYGIVYDLRMHRPLMVQTED 1286
                                                                                                                RKSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKUVSFDIMNIVTQMRKQRCGMIQTKB
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C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1
C;Superfamily: protein, phosphoric monoester hydrolase; tyrosine-specific
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific
E;25-304/Domain: protein 4.1 membrane-binding domain homology <841>
E;922-1157/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1109/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1115/Binding site: substrate phosphate (Arg) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics: <PTP2E>
A;Note: clone PTP2E
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A; Residues: 840-1175
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A;Residues: 1-1175 <LAA>
A;Cross-references: EMBL:U17971; NID:g662113; PIDN:AAA62153.1; PID:g602255
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146; Conserve
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                                             LKGFLSYLEEIQSVRRHTNSTSEPRSPNPPLLVHCSAGVGRTGVVILSBIMVACLEHNBV
                                                                                                ADFFIKYVRYV----RKSHITG--
                                                                                                                                                                                     LEFEHPSVFLETFHVTQYF-----TVRVFQIVKKSTGKSQCVKHLQFTKWFDHGTPAS
                                                                                                                                                                                                                                        SVSGIEWDYIATOGPLONTCODFWOMVWEOGVAIIAMVTABEEGGREKSFRYWP----R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFSDKVKQEGTEEQGSGGYSHKKSLSDATMLIH----SSEEDB---DLEDDSSREHAVSB 729
                                                                                                                                                                                                                                                                                                                                      EYERILKKRLVDGECSTARLPENAERNRFQDVLPYDDARVELVPTKENNTGYINASHIKV
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  FDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQN 458
                                                                                                                                           LGSRHNTVTYGRFKITTRFRTDSGCYATTGLKMKHLLTGQERTVWHLQYTDWPEHGCPED 1074
                                                                                                                                                                                                                                                                                   VNHEEEYFYIATOGPLPETIEDFWOMVLENNCNVIAMITREIECGVIKCYSYWPISLKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                 MKKTRADAKKIGPLKLAALNGLSLSRLPLPDEGKEVSTRATNDERCKVLEQRLEQGTVFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -KKEELDIIR------EFLELEQMTLPDDFNSGNTL----------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SVSEKELTQLAQIRPLIFNSSARSAMRDCL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRITAAFSQEQQLNYPCASVTPVTGPLHIFEPKSHVTBPEKRAKDISPVHLVMETHQPRR 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSSTAG-----PSKTYSPY-----LSGSSRLSKD-----TET----
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                                                                                                                                                                                                                                                                                                                                                                              -QNRDKNRYRDILPYDSTRVPLGKNKD----YINASYIRI
                                                                                          --- PLLVHCSAGVGRTGVFICVDVVFSAIEKWYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 161;
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                 protein-tyrosine-phosphatase (EC 3.1.3.48) - C;Species: Gallus gallus (chicken) C;Date: 13-Sep-1996 #sequence_revision 13-Sep C;Accession: I50212 R;Stoker, A.W.
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A;Accession: T23308
A;Status: preliminary; translated from
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A;Residues: 1-1156 <WIL>
A;Cross-references: EMBL:Z69664; PIDN:CAA93513.1; GSPDB:GN00022;
A;Experimental source: clone K04D7
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_rev
C;Accession: T23308
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                                                                                                                                                                                                                                                                                                                                 DHGVPSSVFPLLSFVHYTSDIHSTGPVVVHCSAGVGRSGSYILVD---SMRRHLISFRRL
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C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas

C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas

F;148-208/Domain: immunoglobulin homology <IMM1>

F;245-299/Domain: immunoglobulin homology <IMM2>

F;317-399/Domain: fibronectin type III repeat homology <3PR>
F;317-399/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F;881-1499/Domain: protein-tyrosine-phosphatase homology <PPP2>

F;1157-1479/Domain: protein-tyrosine-phosphatase homology <PPP2>

F;1141/Active site: Cys (phosphocysteine intermediate) #status predicted

F;11417/Binding site: substrate phosphate (Arg) #status predicted

F;1432/Active site: Cys (phosphocysteine intermediate) #status predicted

F;1438/Binding site: substrate phosphate (Arg) #status predicted
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;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
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                                                                                                                                                                                                                                                                   1446 SIVLERMRYEGVVĎÍFQTVXMLRTÓP-AMVOTEDEYOFCYQAALEYL 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1386 RTVRQFQFTDWPEQGVPKSGEGFIDFIGQVHKTKEQFGQDGPISVHCSAGVGRTGVFITL 1445
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                                                                                                                                                                                                                                                                                                                                                                          410 DVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKBQYQFCYBIVLEVL 456
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Q06180 mus musculu
P35233 rattus norv
P04157 rattus norv
Q05209 homo sapien
P35236 homo sapien
Q13016 gallus gall
P06800 mus musculu
P16621 drosophila
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UENCE OF 1216-24 SUB-PARCTEAS; G H.Y.; GINTED (JUN-1994 UENCE OF 1279-18: SUB-Brain; LINE-95232528; P. D T. Irie S., K. P-1: a protein t; ence 268:411-415 UENCE OF 1323-18:	MEDLINE-94116679; PubMed=8287977; Maekawa K., Imagawa N., Nagamatsu M. Makawa K., Imagawa N., Nagamatsu M. Maekawa K., Imagawa N., Nagamatsu M., Nagamatsu M., Heldin "Cloning and characterization of PTE with similarities to cytoskeletal-se J. Biol. Chem. 269:24082-24089(1994)	SEQUENCE FROM N.A. (ISOFORM 4 SEQUENCE FROM N.A. (ISOFORM 4 TISSUB-Breast carcinoma; Formal Sequence of the lambda	CT-2001 (Rel. 40, Crea CT-2001 (Rel. 40, Last CT-2003 (Rel. 42, Last CT-2003 (Rel. 42, Last cein-tyrosine phosphata tein-tyrosine phosphata tein-tyrosine phosphata pantase 1) (FAP-1). 13 OR PTPIE OR FTPLI ON 13 OR PTPIE OR FTPLI ON 14 OR PTPIE OR FTPLI ON 15 OR PTPIE OR FTPLI ON 15 OR PTPIE OR FTPLI ON 16 OR PTPIE OR FTPLI ON 17 OR TPIE OR FTPLI ON 18 OR PTPIE OR FTPLI ON 18 OR PTPLE OR FTPLI OR FTPLI OR FTPLI ON 18 OR FTPLI OR FTP	1 UMAN TND HUMAN STANDARD; 12973; Q15159; Q15263; Q152	448 18.4 775 1 447 18.3 1445 1 447 18.2 1304 1 444 18.2 2200 1 443.5 18.2 1026 1 442.5 18.1 359 1 442.5 18.1 359 1 440 18.0 1004 1 439 18.0 593 1 437 17.9 432 1 433.5 17.8 593 1
N.A.  EMBL/GenBank/DDBJ database N.A. (ISOFORM 4).  36343; Reed J.C.; phosphatase that associates	87977; Il protein-tyrosine phospha dd GLGF repeats.";  9066; Heldin CH., Gonez L.J.; on of PTPL1, a protein tyro letal-associated proteins. 89(1994).	ORM 4).  =8071359;  tlocco R., Shen SH.;  te phosphatase with homology to  the band 4.1 family and junct  -22327(1994).  ALTERNATIVE SPLICING.	nence update) otation update) non-receptor type 13 (I IB) (PTP-E1) (hPTPE1) PTPL1) (Fas-associated P1. Craniata; Vertebrata; E	ALIGNMENTS PRT; 2485 AA. 264; Q15265; Q15674; Q16826	PTNC MOUSE PTPG HUMAN CD45 HUMAN LAR CAEEL PTPI CAEEL PTNI HUMAN PTNY RAT PTPX RAT PTPX RAT PTPY RAT PTNA RAT PTNI RAT PTNI RAT PTNI HUMAN PTNI MOUSE PTNI RAT
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RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Korley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Bakkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RT and mouse cDNA sequences.";
RN L Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                VARIANTS PRO-1419 AND MET-1522.

WREDLINE=22323362; PubMed=12436199;
Yoshida S., Harada H., Nagai H., Fukino K., Teramoto A., Emi
"Head-to-head juxtaposition of Fas-associated phosphatase-1 (
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-!- FUNCTION: Regulates negatively FAS-induced apoptosis and
mediated pro-apoptotic signaling.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O =
                                                                                                                                                                                                                                                                           Kozlov G., Banville D., Gehring K., Ekiel I.;
"Solution structure of the PDZ2 domain from cytosolic human
phosphatase hPTPIE complexed with a peptide reveals contribution
the beta2-beta3 loop to PDZ domain-ligand interactions.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kozlov G., Gehring K., Ekiel I.; "Solution structure of the PDZ2 domain from and its interactions with C-terminal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-TERMINUS OF TNFRSF6.
MBDLINE=20170882; PubMed=10704206;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99329089; PubMed=10400701; Shen S.-H., Banville D.; Murthy K.K., Clark K., Fortin Y., Shen S.-H., Banville D.; "ZRP-I, a zyxin-related protein, interacts with the second of the cytosolic protein tyrosine phosphatase hPTPIE."; J. Biol. Chem. 274:20679-20687(1999).
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                 tyrosine + phosphate.
SUBUNIT: Interacts with TRIP6 and TNFRSF6
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Peingold E.A., Grouse L.H., Derge J.G.
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EMBL/GenBank/DDBJ databases.
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GO; GO:0004725; F:protein tyrosine phosphatase act
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R InterPro; IPR000299; Band 4:1.
R InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000387; TYR phosphatase.
R InterPro; IPR000387; TYR phosphatase; 1.
R InterPro; IPR000242; Tyr PP.
R PAMET; PR00373; BAND41.
R PRINTS; PR00703; PAND41.
R PRINTS; PR00704; PTPC; 1.
R PROSITE; PS00660; PERM 1; FALSE NEG.
R PROSITE; PS00661; PERM 3; 1.
R PROSITE; PS00661; PERM 3; 1.
R PROSITE; PS00661; PERM 3; 1.
R PROSITE; PS00383; TYR PHOSPHATASE 1; FALSE NEG.
R PROSITE; PS00383; TYR PHOSPHATASE 1; PALSE NEG.
R PROSITE; PS00383; TYR PHOSPHATASE 7; 1.
R PROSITE; PS0055; TYR PHOSPHATASE 7; PALSE NEG.
R PROSITE; PS0055; TYR PHOSPHATASE 7; PALSE NEG.
R PROSITE; PS0055; TYR PHOSPHATASE 7; 1.
R PROSITE; PS0055; TYR PHOSPHATASE 7; PALSE NEG.
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EMBL; D21211; BAA04752.1; -.
EMBL; X80289; CAA56264.1; -.
EMBL; X9078; CAA56264.1; -.
EMBL; X9078; CAA5624.1; -.
EMBL; L34583; AAC41755.1; -.
EMBL; L34583; AAC41755.1; -.
EMBL; A623323; AAC6374.1; -.
EMBL; A623323; AAC6374.1; -.
EMBL; BC03610; AAH39610.1; ALT_TERM.
PIR; A54971; A54971.
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PIB; 3PDZ; 17-MAR-00.
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SIMILARITY: Contains 5 PDZ/DHR domains.
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Non-receptor class subfamily.
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  (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTINE HUMAN STANDARD; PRT; 1187 AA 0,15678; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update. Protein tyrosine phosphatase, non-receptor (Protein-tyrosine phosphatase pez).
                   This SWISS-PROT entry is copyright. It is produced through a copyred the swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by mon-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 209:959-965(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Breast carcinoma;
MEDLINE=95251727; PubMed=7733990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ezrin-like domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crompton M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                  tyrosine + phosphate.
TISSUE SPECIFICITY: Expressed in a variety of human tiss including kidney, skeletal muscle, lung and placenta.
SIMILARITY: Contains 1 FERM domain.
SIMILARITY: Belongs to the protein-tyrosine phosphatase Non-receptor class subfamily.
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GO; GO:0006470; P:protein amino acid de
InterPro; IPR000299; Band 4.1.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000242; Tyr Pp.
Pfam; PF00373; Band 41; I.
Pfam; PF00102; Y phosphatase; 1.
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PRINTS; PR00935; BAND41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00660; FERM 1; 1.

PROSITE; PS00661; FERM 2; 1.

PROSITE; PS00050; FERM 3; 1.

PROSITE; PS00383; TYR PHOSPHATASE 1; 1.

PROSITE; PS00385; TYR PHOSPHATASE PTP; 1.

PROSITE; PS50056; TYR PHOSPHATASE 2; 1.

Structural protein; Cytoskeleton; Hydrolase.
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PIR; JC4155; JC4155.
HSSP; P29350; 1GWZ.
Genew; HGNC:9647; PTPN14.
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                                                                                                                                                                                                                                         HVTQYPTVRVFQIVKKST-----GKSQCVKHLQFTKWPDHGTPASADFFIKY----
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REQRMEMIQTIAQYKEVYQVLIQELQN
                                            RKORCGMIQTKEQYOFCYBIVLEVLON 458
                                                                                              OSVRRHTNSMLEGTKNRHPPIVVHCSAGVGRTGVLILSELMIYCLEHNEKVEVPMMLRLL
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                                                                                                                                        -- VRYVRKSHITG-----PLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQM
                                                                                                                                                                                             KVTTKF--RTDSVCYATTGLKVKHLLSGQBRTVWHLQYTDWPDHGCPEDVQGFLSYLBEI
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amino acid dephosphorylation;
_4.1.
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Pred. No. 7.1e-29;
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PHOSPHOCYSTEINE INTERMEDIATE
(BY SIMILARITY).
POLY-PRO.
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RESULT 3
PTN3\_HUMAN
ID PTN3\_H
AC P26045
DT 01-MAY

HUMAN

STANDARD;

913 \$

P26045; 01-MAY-1992

(Rel.

Created)

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MIM; 176877; -. GO:0004725; F:protein tyrosine phos GO; GO:0006470; P:protein amino acid de InterPro; IPR000299; Band 4.1.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
Pfam; PF00373; Band 41; I.
Pfam; PF00373; Band 41; I.
Pfam; PF00102; Y_phosphatase; 1.
PFAM; PF00102; Y_phosphatase; 1.
PRINTS; PR00935; BAND41.
SMART; SM00295; B41; 1.
SMART; SM00296; B41; 1.
SMART; SM00296; PDZ; 1.
SMART; SM00296; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWIS
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MEDLINE=91296738; PubMed=1648/25;
Yang Q., Tooks N.K.;
"Isolation of a cDNA clone encoding a human protein-tyrosine
"Isolation of a cDNA clone encoding a human protein-tyrosine with homology to the cytoskeletal-associated proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M64572; AAA35647.1; -.
EMBL; S39392; AAB22439.2; -.
EMBL; S76309; AAB33583.1; -.
EMBL; A41109; A41109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphatase with homology to the cytoskeletal-as band 4.1, ezrin, and talin."; proc. Natl. Acad. Sci. U.S.A. 88:5949-5953(1991)
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10-OCT-2003 (Rel. 42, Last annotation update)
Protein tyrosine phosphatase, non-receptor ty
(Protein-tyrosine phosphatase H1) (PTP-H1).
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Genew; HGNC:9655; PTPN3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colon."
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Imai K., Yachi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92327504;
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Bukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTPN3 OR PTPH1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 194-896 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gastroenterol. 29:727-732(1994).
- FUNCTION: May act at junctions between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine + phosphate.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the protein-tyrosine
Non-receptor class subfamily.
SIMILARITY: Contains 1 FERM domain.
SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation burpean Bloinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no waitified and this statement is not removed. Usage by and for commercial contents are not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Protein tyrosine
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"r+oh F., Takekawa
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Primates;
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Matches 119
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O62130;
O62130;
O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
O1-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein tyrosine phosphatase, non-receptor ty
'Protein-tyrosine phosphatase PTP36).
                                                                                                                  SEQUENCE FROM N.A.

STRAIN=CB-17-SCID; TISSUB=Thymus;

STRAIN=CB-17-SCID; TISSUB=Thymus;

MEDLINE=94354845, PubMed=8074693;

Sawada M., Ogata M., Fujino Y., Hamaoka T.;

Sawada M., Ogata M., Hamaoka T.;

Sawada M., Ogata M., Fujino Y., Hamaoka T.;

Sawada M., Ogata M., Hamaoka T.;

Sawada 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa;
Mammalia; Butheria;
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non-hematopoietic origins.
SIMILARITY: Contains 1 FERM domain.
SIMILARITY: Belongs to the protein-
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IE; PS00661; FERM_2; 1.
IE; PS50057; FERM_3; 1.
IE; PS50106; PDZ; 1.
IE; PS50106; TYR_PHOSPHATASE_1; 1.
IE; PS50056; TYR_PHOSPHATASE_2; 1.
IE; PS50056; TYR_PHOSPHATASE_1; 1.
IE; PS50056; TYR_PHOSPHATASE
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Rodentia;
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Pred. No. 9
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Sciurognathi; Muridae;
            protein-tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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InterPro; IPR000299; Band 4.1.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; TYr_pp.
Pfam; PF00102; Y_phosphatase; 1.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00935; BAND41.
PRINTS; PR00906; PRTYPHPHTASE.
PRINTS; PR00700; PRTYPHPHTASE.
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PROSITE; PS00660; FERM
PROSITE; PS00661; FERM
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B; PS00661; FERM 2; 1.
B; PS00661; FERM 3; 1.
B; PS00383; TYR PHOSPHATASE 1; 1.
B; PS00383; TYR PHOSPHATASE 2; 1.
B; PS50056; TYR PHOSPHATASE 2; 1.
ural protein; Cytoskeleton; Hydrolase.
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                                                                                                                                                                                                                                                                                                                         BESYFYIATQGPLPETIEDFWOMVLENNCNVIAMITREISCGVIKCYSYWPISLKEPLEF
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IMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQN
                                                                                                          FIKY----VRYVRKSHITG-----
                                                                                                                                                              KHSSATYGKFKVTTKFRTDSGCYATTGLKVKHLLSGQERTVWHLQYTDWPHHGCPEDVQG
                                                                                                                                                                                                                                                                      GSEWHY LATQGPLPHTCHDFWOMVWEQGVNVLAWVTAESEGGRTKSHRYWP-----KLGS
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                                                      FLSYLEEI QSVRRHTNSVLEGIRTRHPPI VVHCSAGVGRTGVVILSELMIYCLEHNEKVE
                                                                                                                                                                                                               EHFSVFLETFHVTQYF-----TVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADF
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Pred. No. 2.6e-27;
4; Mismatches 125
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POLY-GLY.
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                                                                                               PLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFD
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458
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RESULT

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[4]
SEQUENCE OF 1503-1589 FROM N.A.
SEQUENCE OF 1503-1589 FROM N.A.
Arimura Y.,
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Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Banganan L., Erler A., Christensen M., Georgescu A., Avila J., Liv
Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kromniller B.,
Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Olsen A.S., Carrano A. V.;
"Sequence analysis of a 2.5 Mb region in 19p13.3.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Protein-tyrosine phosphatase expression in Cancer Res. 52:737-740(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adachi M., Seki
Imai K., Yachi
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MEDLINE=96255038; PubMed=8992885;

MEDLINE=96255038; S.J., Opas E.E., Vogel R.

Endo N., Rutledge S.J., Opas E.E., Vogel R.

"Human protein tyrosine phosphatase-sigma:
inhibition by bisphosphonates.";
1. Bone Miner. Res. 11:535-543(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96102179; PubMed=8524829;
Pulido R., Serra-Pages C., Tang M., Streuli M.;
Pulido R., Serra-Pages C., Tang M., Streuli M.;
"The LAR/Fprg delta/Fpr sigma subfamily of transmembrane protein-
tyrosine-phosphatases: multiple human LAR, FTP delta, and FTP sigma
tyrosine-phosphatases: multiple human LAR, FTP delta, and FTP sigma
tsoforms are expressed in a tissue-specific manner and associate with
the LAR-interacting protein LIP.1.";
Proc. Natl. Acad. Sci. U.S.A. 92:11686-11690(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSUE=Fetal brain;
placenta and liver.

SIMILARITY: BELONGS TO THE RECEPTOR CLASS OF THE PROTEIN-TYPE PROSPHATASE FAMILY.

SIMILARITY: Contains 3 immunoglobulin-like C2-type domain.

SIMILARITY: Contains 8 fibronectin type III domains.

SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                 IsoId=013332-5; Sequence=VSP 050023, VSP 050025; TISSUE SPECIFICITY: Detected in all tissues tested
                                                                                                                                      Name=PTPS-F4-7;
IsoId=Q13332-5;
                                                                                                                                                                                                                                                                                                                                             tyrosine + phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Interacts with LAR-interacting protein CATALYTIC ACTIVITY: Protein tyrosine phosphate +
                                                                                                                                                                                         IsoId=Q13332-3; Sequence=VSP_050022,
Name=PTPS-MEC;
                                                                                                                                                                                                                              Name=PTPS-MEB;
                                                                                                                                                                                                                                           Name=PTPS-MEA;
IsoId=Q13332-2;
                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=5;
                                                                                                                                                                  IsoId=Q13332-4; Sequence=VSP_050024;
                                                                                                                                                                                                                                                                              IsoId=Q13332-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                  Comment=Additional
                                                                                                                                                                                                                                         Sequence=VSP_050021;
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                                                                                                                                                                                                                                                                                                                  seem to
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,
                                                                                                                                                                                                     VSP_050026,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ., Rodan G.A., Schmidt alternative splicing
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                                                                                PROTEIN-TYROSINE
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MIM; 601576;

GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005001; F:transmembrane receptor protein tyros
InterPro; IPR008957; FN III-like.
InterPro; IPR003961; FN III.
InterPro; IPR003962; Fn III.
InterPro; IPR003962; Fn III.
InterPro; IPR003598; Ig_c2.
R InterPro; IPR003598; Ig_c2.
R InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000342; Tyr_PP.
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SMART; SM00194; PTDC; 2.
SMART; SM00194; PTDC; 2.
PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS500383; TYR_PHOSPHATASE_2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
PROSITE; PS50056; TYR_PHOSPHATAS
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EMBL; U40317; AAC50567.1; -
EMBL; AC005790; AAC6233.1; -
EMBL; S78080; AAB21146.2; -.
HSSP; P18052; 1YFO.
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PRINTS; PR007014; FNTYPEJII.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00060; FN3; 7.
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PF00047; ig; 3
PF00102; Y_phc
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CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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PIBRONECTIN TYPE-III
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                                                                                                                                                          PHOSPHOCYSTEINE INTERMEDIATE SIMILARITY).
               Missing (in isoform /FTId=VSP_050021
                                                   N-LINKED
                                                                                                                       PHOSPHOCYSTEINE INTERMEDIATE SIMILARITY).
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isoform PTPS-MEB)
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Homo sapiens (Human).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
NCBI\_TaxID=9606;

Chordata; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

(EC 3.1.3.48) (MEG).

SEQUENCE FROM N.A.

MEDIINE=91288564; PubMed=1648233; Gu M., York J.D., Warshawsky I., Majerus "Identification, cloning, and expression protein-tyrosine-phosphatase with sequence

Majerus P.W.; ression of a cytosc sequence homology

cytosolic

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cytoskeletal megakaryocyte

SEQUENCE FROM N.A.

Proc. protein

Natl. Acad. Sci.

U.S.A.

88:5867-5871(1991)

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Best Local Sim
Matches 108;
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P29074;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 4
Protein tyrosine phosphatase MEG1) (FTPase-MEG1)
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T -> HP (IN REF. 2).
SA -> RP (IN REF. 2).
LGPV -> RSPA (IN REF. 2).
GAZGRGPPR -> REARGRRS (IN REF. 2).
R -> P (IN REF. 2).
AAEPGAENAV -> GRLSRAFRTL (IN REF. 2).
TV -> SL (IN REF. 2).
F -> S (IN REF. 2).
E -> D (IN REF. 4).
V -> K (IN REF. 4).
V -> K (IN REF. 2).
N -> K (IN REF. 2).
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Pred. No. 5.3e-27;
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RC HISSUE-COLORS; PubMed-1247932;

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Best Local
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Q12913; Q15255; Q8NHM2;
Q12913; Q15255; Q8NHM2;
Q1-NOV-1997 [Rel. 35, Created)
10-OCT-2003 [Rel. 42, Last sequence update)
10-OCT-2003 [Rel. 42, Last annotation update)
Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (
(HPTP eta) [Protein-tyrosine phosphatase receptor type J)
(HPTP eta) [Protein-tyrosine phosphatase receptor type J)
                                                     SEQUENCE
PRO-276.
                                                                                                                                                                                                                                                                                   MEDILINE=95024024; PubMed=7937872;
Oestman A., Yang Q., Tonks N.K.;
Oestman A., Yang Q., Tonks N.K.;
"Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase,
is enhanced with increasing cell density.";
proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).
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                                                                                                                  MEDIINE=95086212; PubMed=7994032;
Honda H., Inzawa J., Nishida J., Yaz
Molecular cloning, characterization,
a novel protein-tyrosine phosphatase,
plood 84:4186-4194(1994).
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Eukaryota; Metazoa;
Mammalia; Butheria;
                            TISSUE=Colon,
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     PubMed=12089527;
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Primates;
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Pred. No. 9.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                            AND
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                                                                                                                                                                                            Yazaki Y.,
                                                                            VARIANTS
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                                                                                                                                              eta.";
                                                                            COLON
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Pfam; PF00041; fn3; 6.

Pfam; PF00102; Y_Dhosphatase; 1.

PRINTS; PR00700; PRTYPHPHTASE.

SMART; SM00060; FN3; 8.

SMART; SM000194; FTPG; 1.

PROSITE; PS000383; TYR_PHOSPHATASE 1; 1.

PROSITE; PS00056; TYR_PHOSPHATASE_PTP; 1.

PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
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EMBL; AP307828; AAM69432.1

EMBL; AP307829; AAM69432.1

EMBL; AP307830; AAM69432.1

EMBL; AP307831; AAM69432.1

EMBL; AP307831; AAM69432.1

EMBL; AP307833; AAM69432.1

EMBL; AP307834; AAM69432.1

EMBL; AP307834; AAM69432.1

EMBL; AP307835; AAM69432.1

EMBL; AP307836; AAM69432.1

EMBL; AP307840; AAM69432.1

EMBL; AP307840; AAM69432.1

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EMBL; AP307840; AAM69432.1

EMBL; AP307842; AAM69432.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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                                                                                                                                                                                                         GO:0005087; C:integral to plasma membrane; TAS.
GO:0005081; F:transmembrane receptor protein tyrosine pho.
GO:0007001; P:cell-cell signaling; TAS.
GO:0007267; P:cell-cell signaling; TAS.
; GO:0007470; P:protein amino acid dephosphorylation; TAS.
; GO:0007169; P:transmembrane receptor protein tyrosine kin.
terPro; IPR003951; FN III.
terPro; IPR003961; FN III.
terPro; IPR00397; TVF phosphatase.
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SIMILARITY: Contains 1 protein-tyrosine phosphatase contains.

SIMILARITY: Contains 5 fibronectin type III domains.

DATABASE: NAME=PROW; NOTE=CD guide CD148 entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd148.htm".
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SUBCELLULAR LOCATION: Type I membrane protein.
PTM: N- and O-glycosylated.
DISBASE: Defects in PTPRJ are found in cancers of colon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Protein tyrosine phosphate +
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AF387824; AAM69432.
AF387825; AAM69432.
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D37781; BAA07035.
AF387844; AAM6943
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RP SEQUENCY
RC STRAU
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                                                        InterPro; IPR000299; Band 4.1.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000242; TYP PP.
Pfam; PF00373; Band 41; I.
Pfam; PF00102; Y phosphatase; 1.
PRINTS; PR00935; BAND41.
PRINTS; PR00900; PRTYPHPHTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTINL RAT STANDARD; PRT; 1175 AA. 662728; Q62732; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Protein tyrosine phosphatase, non-receptor type (Protein-tyrosine phosphatase 2E). PTPN21 OR PTP2E.
                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Sprague-Dawley;

MEDLINE=95104449; PubMed=7805871;

L'Abbe D. Banville D. Tong Y. Stocco R., Mentus G. Shen S.H.;

"Identification of a novel protein tyrosine phomology to the cytoskeletal proteins of the FEBS Lett. 356:351-356(1994)

-i- CATALYTIC ACTIVITY: Protein tyrosine phos
  PROSITE;
                                                                                                                                                                                                          EMBL; U17971; AAA62153.1;
EMBL; U18293; AAA62154.1;
PIR; S51005; S51005.
HSSP; Q06124; 2SHP.
                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q62728-2; Sequence=VSP 000498; TISSUE SPECIFICITY: Particularly abundantly in adrenal g SIMILARITY: Contains 1 FERM domain. SIMILARITY: Belongs to the protein-tyrosine phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Non-receptor class subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=2
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                      SM00295;
SM00194;
  PS00660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKE
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                      : B41; 1.
FERM_1; 1.
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Sciurognathi; Muridae;
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Murinae; Rat
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Matches
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Best Local :
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PROSITE; PS50057; FERM 3; 1.

PROSITE; PS50057; TYR PHOSPHATASE PTP; 1.

PROSITE; PS50055; TYR PHOSPHATASE PTP; 1.

PROSITE; PS50056; TYR PHOSPHATASE PTP; 1.

PROSITE; PS50056; TYR PHOSPHATASE PTP; 1.

Structural protein; Cytoskeleton; Hydrolase; Al

DOMAIN 23 308

DOMAIN 922 1175

PROTEIN-TYROSINE P

ACT_SITE 1109 1109

PHOSPHOCYSTEINE INTERV
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                                                                                                       ADFFIKYVRYV----RKSHITG------PLLVHCSAGVGRTGVFICVDVVFSAIBKNYS
                                                                                                                                                                                       LEPEHFSVFLETFHVTQYF-----TVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPAS
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  LDIPRVLELLRQQRMMLVQTLSQYTFVYRVLIQFLKS
                                     PDIMNIVIQMRKORCGMIQTKEQYOFCYBIVLEVIQN
                                                                            LKGFLSYLEBIQSVRRHTNSTSEPRSPNPPLLVHCSAGVGRTGVVILSEIMVACLEHNEV
                                                                                                                                                       LGSRHNTVTYGRFKITTRFRTDSGCYATTGLKMKHLLTGQERTVWHLQYTDWPEHGCPED
                                                                                                                                                                                                                                                                        VNHEBEYFYIATOGPLPETIEDFWOMVLENNCNVIAWITREIECGVIKCYSYWPISLKEP
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                                                                                                                                                                                                                                                                                                                                                                                            MKKTRADAKKIGPIKLAALNGISISRIPIPDEGKEVSTRATNDERCKVLEQRIEQGTVFT
                                                                                                                                                                                                                                                                                                                                                                                                                                    -KKEBLDIIR-----EFLELEQMTLPDDFNSGNTL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SVSEKELTQLAQIRPLIFNSSARSAMRDCL------
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PTPRK OR PTPK.
Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; P
                                                                                                                                                              Q15262; Q14763;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Receptor-type protein-tyrosine phosphatase ka
(EC 3.1.3.48) (R-PTP-kappa).
SEQUENCE FROM N.A.
MEDLINE=96279245; PubMed=8663237;
Fuchs M., Mueller T., Lerch M., U
                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                                                                                                                                               PTPK_HUMAN
                                                                                                                                                                                                                                                                               STANDARD;
                                                                                           Chordata;
Primates;
                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                               PRT;
     Ullrich
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     A
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                                                                                                                                                                                    kappa
                                                                                                                                                                                      precursor
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R Genew, HCMC:9674; PTPRK.

R GGenew, HCMC:9674; PTPRK.

R GO; GO:005081; C:integral to plasma membrane; TAS

GO; GO:005081; F:transmembrane receptor protein t

InterPro; IPRO08957; FN_III_like.

InterPro; IPRO08957; FN_III_like.

R InterPro; IPRO0359; IG.

R InterPro; IPRO0359; IG.

R InterPro; IPRO00387; TYR_phosphatase.

R InterPro; IPRO00242; TYR_phosphatase.

R InterPro; IPRO00242; TYR_phosphatase.

R InterPro; IPRO00242; TYR_phosphatase.

R Pfam; PF00047; iG; 1.

R Pfam; PF00047; iG; 1.

R Pfam; PF00002; Y_phosphatase; 2.

R Pfam; PF000102; Y_phosphatase; 2.

R Pfam; PF00020; MAM, DOMAIN.

R PFAMT; PR00700; PRTYPHPHTASE.

R SMART; SM00104; FTS; 1.

R SMART; SM00194; PTPC; 2.

R PROSITE; PS00836; MAM_2; 1.

R PROSITE; PS00836; MAM_2; 1.

R PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.

P PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
                       Immunoglobul
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Association of human protein-tyrosine phosphatase kappa with members of the armadillo family.";
J. Biol. Chem. 271:16712-16719(1996).
                                                           PROSITE; PO
PROSITE; PO
Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97199372; PubMed=9047348; Yang Y., Gil M.C., Choi B.Y., Park S.H., Pyun K.H., Ha H.; Yang Y., Gil M.C., Choi B.Y., Park S.H., Pyun K.H., Ha H.; "Molecular cloning and chromosomal localization of a human homologous to the murine R-PTP-kappa, a receptor-type prote
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z70660; CAA94519.1; -.
EMBL; L77886; AAC37599.1; -.
HSSP; P28827; 1RPM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine phosphatase.";
Gene 186:77-82(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: This protein undergoes proteolytic processing.
SIMILARITY: Contains 1 MAM domain.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
SIMILARITY: Contains 4 fibronectin type III domains.
SIMILARITY: Contains 2 protein-tyrosine phosphatase domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kappa.
CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Regulation of processes involving cell contact and adhesion such as growth control, tumor invasion, and metastasis. Forms complexes with beta-catenin and gamma-catenin/plakoglobin. Beta-catenin may be a substrate for the catalytic activity of PTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              junctions.
TISSUE SPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine + phosphate
                                                    SMODITY, ...
SMODITY, ...
E; PS50835; IG LIKE; 1.
E; PS50740; MAM 1; 1.
E; PS50060; MAM 2; 1.
IE; PS500383; TYR PHOSPHATASE 1; 2.
IE; PS500383; TYR PHOSPHATASE 2; 2.
TE; PS50056; TYR PHOSPHATASE PTP; 2.
TE; PS50056; TYR PHOSPHATASE PTP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIFICITY: High levels in lung, brain pancreas, stomach, kidney, placenta and
                                                 Receptor; G
27
                        27
                                             tor; Glycoprotein; ?
                        1439
           POTENTIAL.
RECEPTOR-TYPE PROTEIN-TYROSINE PHOSPHATASE KAPPA.
 EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                          protein
 (POTENTIAL)
                                                               Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                        TAS.
                                                                                                                                                                                                                                                                                                                                                                          tyrosine
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Best Local
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CONFLICT
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CARBOHYD
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  1100
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                                                                                                                                                                                                                                                                                                                                                                                                                  135;
                                                                                                                                                                                                                                                                                                                                      77
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                    TRVPL----GKNKDYINASYIRIVNHEBEYFYIATQGPLPETIEDFWQMVLENNCNVIA
  DMAEREGVVDIYNCVKALRSRRINMVQTEEQYIFIHDAILE
                        SAIEKNYSFDIMNIVTOMRKORCGMIQTKEOYOFCYBIVLE 454
                                                              VKHLQFTKWEDHGTBASADFEIKYVRXYRKSH--ITGELLVHCSAGVGRTGVFICVDVVF
                                                                                                    WVTNLVEVGRVKCYKYWPDDTBVYGDFKVTCVEMBPL---AEYVVRTFTLERRGYNEIRE
                                                                                                                         MITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETEHVTQYFTVRVFQIVKKSTGKSQC
                                                                                                                                                      SRVILQPVEDDPSSDYINANYID--GYQRPSHYIATQGPVHETVYDFWRMIWQEQSACIV
                                                                                                                                                                                                      DCLNTLQKKEBLDIIREFLELEQMTLPDDFNSGNTL------QNRDKNRYRDILPYDS
                                                                                                                                                                                                                                                             ENHSATABS
                                                                                                                                                                                                                                                                           RWNSMDSETAGPSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFNSSARSA-MR
                                                                                                                                                                                                                                                                                                             KSKLAKKRKDAMGNTRQEMTHMVNAMDRSYADQSTLHAEDPLSI----TFMDQHNFSPRY
                                                                                                                                                                                                                                                                                                                                                                                        EEEGNSGNLNLRNSLPSSSQKWTPTKPVQNKNLMKYEEHLDILMVFLLIKTIWYNVFKLW
                                                                                                                                                                                                                                                                                                                                     KGKLIFGNK--MNSENVKPSHHL----SFSDKYELVYPEPLESDTDETVWDVSDRSLRN
                                                                                                                                                                                                                                                                                                                                                              EKETKTQCVRIATKAATEEPEVIPDPAKQTDRVVKIAGISAGILVPILLLLVVILIVK--
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775
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1200
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9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 483.5; DB
; Pred. No. 3e-26;
83; Mismatches 1
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FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
PROTEIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYTROSINE PHOSPHATASE 2.
PHOSPHOCYSTEINE INTERMEDIATE (I
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N-LINKED
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CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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DOMAIN

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RESULT 10
PTPT HUMAN
ID PTPT HUMAN
S:
AC 014572; 043655; 0
AC 09UBD2; 09UUL7;
   RA Deloukas P., Matthess L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almedda J.P., Babage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Bailey J.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Chepman J.C., Clamp M., Clark G., Clark M.N., Clark S.Y., Clee C.M.,
RA Chepman J.C., Clamp M., Clark G., Clark M.N., Clark S.Y., Clee C.M.,
RA Cleeg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clington A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Bilington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Graiham D.V., Griffiths C., Criffiths M.N.D., Gwilliam R., Hail R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Hamberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Milme S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milme S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Rice C.M., Ross M.T., Scott C.E., Sebra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Beck S.,
RA ROSers J.
RPTPrho
BMC Geno
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor-type protein-tyrosine phosphatase T (R-PTP-T) (RPTP-rho).
                                                                  Besco J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21638749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  suitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97323006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mu/kappa-like receptor protein tyrosine phosphatase
is restricted to the central nervous system.";
Brain Res. Mol. Brain Res. 56:9-21(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McAndrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTPRT OR KIAA0283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Construction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McAndrew P.E., Frostholm A., White R.A., Rotter A., "Identification and characterization of RPTP rho, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98267260; PubMed=9602027;
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                                                  "Genomic
                                                                                                     ALTERNATIVE
                   Genomics
                                                                                                                                   WA sequence and comparative analysis of human chromosome
414:865-871(2001).
                              genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Nagase T., Ishikawa K.-I.,
Nomura N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4:53-59 (1997)
                                                    organization and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tor analysis
                                              30707; PubMed=11423001;
Frostholm A., Popesco M.C.,
Ganization and alternative s
                                                                                                   SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A.
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; 075664; Q9BR24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=11780052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  characterization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1463
1; Q9BR28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND CHARACTERIZATION
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                                                  splicing of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                precursor
                                                  of the human
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novel RPTP
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C
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                                                                    Rotter A.;
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                                                    and
                                                                                                                                                     20. ";
                                                    mouse
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Pfam; PP00041; fn3; 3.1—1.

Pfam; PP00629; MAM; 1.

Pfam; PP00102; Y_Dhosphatase; 2.

Pfam; PP00102; Y_Dhosphatase; 2.

PRINTS; PR00102; MAMDOWAIN.

PRINTS; PR00700; PRTYPHPHTASE.

PRINTS; SM00060; PN3; 3.

SMART; SM00104; PTPC; 2.

SMART; SM00104; PTPC; 2.

SMART; SM00104; PTPC; 2.

SMART; SM00104; PTPC; 1.

PROSITE; PS00355; IGLIKE; 1.

PROSITE; PS00355; IGLIKE; 1.

PROSITE; PS00363; TYR_PHOSPHATASE 1; 2.

PROSITE; PS00363; TYR_PHOSPHATASE PTP; 2.

PROSITE; PS00055; TYR_PHOSPHATASE PTP; 2.

PROSITE; PS00055; TYR_PHOSPHATASE PTP; 2.
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or send a
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EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                       GG; GO:0007169; P:transmembrane recep
InterPro; IPR003961; FN_III.
InterPro; IPR007110; Ig-like.
InterPro; IPR000998; MAM_domain.
InterPro; IPR000399; PTPC_motif.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P28827; 1RPM.

Genew; HGNC:9682; PTPRT.

GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0005901; F:transmembrane receptor protein tyrosine pho.

GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.

GO; GO:0007169; P:transmembrane receptor protein tyrosine kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BMC Genomics 2:5-5(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERRATUM.
MEDLINE=22730717; PubMed=11814386;
                                              CHAIN
                DOMAIN
 TRANSMEM
                                                               SIGNAL
                                                                                           Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: May be involved in both signal transduction and cellula adhesion in the CNS.

CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=014522-2; Sequence=VSP_007802;
TISSUE SPECIFICITY: Expression is restricted to the CNS.
SIMILARITY: Contains 1 MAM domain.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
SIMILARITY: Contains 4 fibronectin type III domains.
SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L; AF043644; AAD09421.2; -...
(; AB006621; BAA22952.2; ALT_
L; AL021395; CAC24740.2; -...
L; AL022339; CAC26785.1; -...
L; AL0224473; CAA19666.1; -...
L; AL031656; CAB51752.1; -...
L; AL049812; CAB92429.1; -...
L; AL049812; CAB91828.1; -...
L; AL1316461; CAB91828.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine + phosphate.
SUBCELLULAR LOCATION: Type I membrane
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Name=1;
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AL136461;
Z93942; CA
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                                                                            Receptor; (
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767
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1463
                                                                                         Glycoprotein;
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Repeat; Alternative
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              POTENTIAL.
RECEPTOR-TYPE F
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EXTRACELLULAR
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                                                                            Transmembrane; splicing.
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NLVQTEEQYVEVHDAILE
                                                               FVRQVKFLNPPEAGPIVVHCSAGAGRTGCFIAIDTMLDMAENEGVVDIFNCVRELRAQRV 1146
                                                                                         YVRYVR--KSHITGPLLVHCSAGVGRTGVFICVDVVPSAIEKNYSFDIMNIVTQMRKQRC
                                                                                                                             YGDIK--VTLIETEPLAEY-VIRTFTVQKKGYHEIRELRLFHFTSWPDHGVPCYATGLLG
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N-LINKED (GLCNAC.

Missing (in isoform 2
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P -> A (IN REF. 3)
T -> W (IN REF. 1)
A -> P (IN REF. 1)
MISSING (IN REF. 1)
L -> P (IN REF. 1)
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FIBRONECTIN TYPE-III 2
FIBRONECTIN TYPE-III 3
FIBRONECTIN TYPE-III 4
FIBRONECTIN TYPE-III 4
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PROTEIN-TYROSINE PHOSP
PROTEIN-TYROSINE PHOSP
PROTEIN-TYROSINE INTERN
SIMILARITY)
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Pred. No. 4.2e-26;
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DALDER BESCHOOLD BESCHER BESCHOOLD B
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RESULT 11
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EMBL; X54133; CAA38068.1; -
PIR; A56178; A56178.
HSSP; PL8052; 1YFO.
Genew; HGNC:9668; PTPRD.
MIM; 601598; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005901; F:transmembrane receptor protein tyrosin
GO; GO:0006470; P:protein amino acid dephosphorylation;
GO; GO:0007185; P:transmembrane receptor protein tyrosin
InterPro; IPR008957; FN_III-like.
InterPro; IPR003961; FN_III_subd.
InterPro; IPR003962; Fn_III_subd.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine + phosphate.
1- SUBCELLULAR LOCATION: Type I membrane protein
-1- ALTERNATIVE PRODUCTS:
Bvent-Alternative splicing; Named isoforms=3;
Comment-Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krueger N.X., Streuli M., Saito H.;
Structural diversity and evolution of hu
tyrosine phosphatases.";
EMBO J. 9:3241-3252(1990).
-I- CATALYTIC ACTIVITY: Protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M., "Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta. Evidence for tissue-specific expression alternative human transmembrane protein-tyrosine phosphatase delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1991
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Krueger N.X., Streuli M., Saito H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND MUTAGENES
MEDLINE=95204468; PubMed=7896816;
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10-0CT-2003
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SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 8 fibronectin type III domains.
SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
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ame=2; Synonyms=Kidney;
IsoId=P23468-2; Sequence=VSP_005147, VSP_005148,
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hosphorylation; TAS.
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Query Match
Best Local S
Matches 107
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R Pfam; PF00102; Y_Dhosphatase; 2.

R PF1NTS; PR001014; FNTYPEIII.

R PRINTS; PR00700; PRTYPHHTASE.

R PRINTS; SM00408; IG-2; 2.

R SMART; SM00408; IG-2; 2.

R SMART; SM00408; IG-LIKE; 3.

R PROSITE; PS500383; ITR_PHOSPHATASE 1; 2.

R PROSITE; PS500383; TYR_PHOSPHATASE 2; 2.

R PROSITE; PS50056; TYR_PHOSPHATASE 2PP; 2.

R PROSITE; PS50056; TYR_PHOSPHATASE 3PP; 2.
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InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_pp.
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                                 1760
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                                                                                                                           207 LELEQMTLPDD------FNSGNTLQNRDKNRYRDILPYDSTRVPLG-----KNKDYINAS
                                                                                                                                                          107;
                                                                                                                                                                    Similarity
FFIKYVRYVRKSH----ITGELLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQ 430
                               AERSARYQYFVVDEMABYNMPQYI-LREFKVTDARDQQSRTVRQFQFTDWPEQGVFKSGE
                                                                        FID--GYRQQKAYIATQGPLAETTEDFWRMLWEHNSTIVVMLTKLREMGREKCHQYWP--
                                                                                       YIRIVNHEEEYFYIATQGPLPETIEDFWQWVLENNCNVIAMITREIECGVIKCYSYWPIS
                                          LKEPLEFEHFSVF-LETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTFASAD
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MW; 3A
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N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)

Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                    IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 3.
IT-BRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 7.
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/FTId=VSP 005150.
R-sA: 2.5-FOLD REDUCTION IN
MW; 3AE8CECD32182E26 CRC64;
                                                                                                                                                         Score 481.5; DB
Pred. No. 6e-26;
S; Mismatches
                                                                                                                                                                                                                                                    Missing (in isoform 2).
                                                                                                                                                                                                                                                               Missing (in /FTId=VSP_00
                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                    PHOSPHOCYSTEINE INTERMEDIATE
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Missing (In isofo
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                                                                                                                                                                                                                                                               005148
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                                                                                                                                                                            DB 1;
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(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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PRINTS, PR00935; BAND41.

PRINTS, PR00935; BAND41.

PRINTS, PR00700, PRTYPHPHTASE.

SMART; SM00295; B41; 1.

SMART; SM00294; PTPC; 1.

PROSITE; PS00660; FERM 1; 1.

PROSITE; PS00661; FERM 3; 1.

PROSITE; PS00383; TYR_PHOSPHATASE_T; 1.

PROSITE; PS00383; TYR_PHOSPHATASE_PTP; 1.

PROSITE; PS00365; TYR_PHOSPHATASE_PTP; 1.

PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.

PROSITE; PS50056; TYR_PHOSPHATASE_T; 1.

SCRUCTURE PS50056; TYR_PHOSPHATASE_T; 1.

PROSITE; PS50056; TYR_PHOSPHATASE_T; 1.
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Q6213G;
Q6213G;
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 42, Last annotation update)
Q1-CCT_2003 (Rel. 42, Last annotation update)
Q2003 (Rel. 42, Last annotation update)
Q2004 (Rel. 42, Last annotation update)
Q2005 (Rel. 42, Last annotation update)
Q2006 (Rel. 42, Last annotation update)
Q2007 (Rel. 35, Last sequence update)
Q2007 (Rel
                                                      Structural
DOMAIN
DOMAIN
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-C57BL/6; TISSUE-Liver;

MEDLINE-95140431; PubMed-7838537;

Higashitsuji H., Arii S., Furutani M., Imamura M., Kaneko Y.,

Takenawa J., Nakayama H., Fujita J.;

Takenawa J., Naneko Y.,

Takenawa J.,

Takenawa J., Naneko Y.,

Takenawa J.,

Takenawa J., Naneko Y.,

Takenawa J.,

Takenawa
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InterPro; IPR000299; Band 4.1.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_PP.
Pfam; PF00373; Band_41; I.
Pfam; PF00102; Y phosphatase; 1.
PRINT C. PROCOSE: PANTA 1
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PIR; IS8345; I58345.
HSSP; P29350; IGWZ.
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-I- CAPALYTIC ACTIVITY: Protein tyros
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncogene 10:407-414(1995).
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TISSUE SPECIFICITY: Liver.
SIMILARITY: Contains 1 FERM domain.
SIMILARITY: Belongs to the protein-tyrosine
Non-receptor class subfamily.
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PERM.
PROTEIN-TYROSINE PHOSPHATASE.
PHOSPHOCYSTEINE INTERMEDIATE
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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Best Local S
Matches 143
                                                                                                                                                                                                                                                                                  MOUSE STANDARD; PRT; 1457 AA.

PTEK MOUSE STANDARD; PRT; 1457 AA.

P35822;

O1-JUN-1994 (Rel. 29, Created)

O1-JUN-1994 (Rel. 29, Last sequence update)

10-CCT-2003 (Rel. 42, Last annotation update)

10-CCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                 Receptor-type p
(EC 3.1.3.48) (
PTPRK OR PTPK.
                                                                                                                           (1)
SEQUENCE FROM N.A.
STRAIN-RI; TISSUS-Brain;
MEDLINE-93233655; PubMed=8474452;
MEDLINE-93233655, PubMed=8474452;
"Cloning and characterization of R-PTP-kappa, a new member of the receptor protein tyrosine phosphatase family with a proteolytically cleaved cellular adhesion molecule-like extracellular region."; Mol. Cell. Biol. 13:2942-2951(1993).

-i- FUNCTION: Regulation of processes involving cell contact and adhesion such as growth control, tumor invasion, and metastasis. Forms complexes with beta-catenin and gamma-catenin/plakoglobin.

Beta-catenin may be a substrate for the catalytic activity of PTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                      Jiang
Sap J
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                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                   musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1092
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143; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TARLPENAERNRPQDVLPYDDARVBLVPTKENNTGYINASHIKVSVSGIEMDYIATQGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CMIOTKEQYOFCYEIVLEVLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTNSTSEPKSH-NPPLLVHCSÁGVGRTGVVILSBIMVACLEHNEVLDIPRVLDMLRQQRM 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRERIDSGCYATIGLKMKHLLTGQERTVWHLQYTDWPEHGCPEDLKGFLSYLEEIQSVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QYF----TVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QNTCQDFWQMVWEQGVAIIAMVTABEEGGREKSFRYWP-----RLGSRHNTVTYGRFKIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHESVFLETEHVF
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565
1176
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                                                                                                                                                                                                                                                                               protein-tyrosine (R-PTP-kappa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -QNRDKNRYRDILPYDSTRVPLGKNKD----YINASYIRIVMHEEEYFYIATQGPL
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572
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; Pred. No. 3.4e-26;
74; Mismatches 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW; 529FBE22P1335B75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHHLSFSDKYELV----YPEPLESDT--DETVWDVSDRSLR
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POLY-PRO.
                                                                                                                                                                                                                        Craniata; Vertebrata; Buteleostomi; Sciurognathi; Muridae; Murinae; Mus
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G
                                                                                                                                    Musacchio J.M.,
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                                                                                                                                                                                                                                                                                               precursor
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                                                                                                                                      Schlessinger
                                                                                                                                                                                                                           Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00047; in3; 2.

Lam; PF00047; in3; 2.

PFAM; PF00047; in3; 2.

DR Pfam; PF00022; MAM; 1.

DR PFAM; PF00020; MAMCOMAIN.

DR PRINTS; PR00020; MAMCOMAIN.

DR PRINTS; PR00020; MAMCOMAIN.

R RINTS; PR00020; FN3; 2.

R SMART; SM00409; IG; 1

SMART; SM00409; IG; 1

SMART; SM001177
            DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                           DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                         SMART; SM00194; PTPC; 2.

PROSITE; PSS0935; IG LIKE; 1.

PROSITE; PS00740; MAM_1; 1.

PROSITE; PS00760; MAM_2; 1.

PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.

PROSITE; PS00056; TYR_PHOSPHATASE_71P; 2.

PROSITE; PS00056; TYR_PHOSPHATASE_71P; 2.

PROSITE; PS0056; TYR_PHOSPHATASE_71P; 2.

PROSITE; PS0056; TYR_PHOSPHATASE_71P; 2.

PAGFOLAGE; RECEPTOR; Glycoprotein; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003599; Ig.
InterPro; IPR000998; MAM domain.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_PP.
Pfam; PP00041; fn3; 2.
Pfam; PP00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
PIR; A
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PTM: This protein undergoes proteolytic processing.
-!- SIMMILARITY: Contains 1 MAM domain.
-!- SIMMILARITY: Contains 1 immunoglobulin-like C2-type domain.
-!- SIMMILARITY: Contains 4 fibronectin type III domains.
-!- SIMMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                             DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR008957;
InterPro; IPR003961;
InterPro; IPR007110;
                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:103310; Ptprk.
                                                                ACT_SITE
                                                                                           ACT_SITE
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CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = proteining the phosphate + phosphate.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: High levels in liver and kidney. Lower lines protein and heart. Not seen in spleen and testis.

In lung, brain and heart. Not seen in spleen and testis.

DEVELOPMENTAL STAGE: Developmentally regulated with highest protein areas capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression found in developing areas or developmental plasticity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A48066; A48066.
; P28827; 1RPM.
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                                                                                                                                                                                                                                                                                                                 lobulin
                                                                                                          26
                                                                                                                                                                                                                                                                                                                 domain;
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1457
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774
1457
193
280
383
473
578
679
1158
1452
            269
100
139
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FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       īg−like.
                                                                                                                                                                                                                                                                                                                   Repeat
                                                                                              PIBRONECTIN TYPE-III 1.
PIBRONECTIN TYPE-III 2.
PIBRONECTIN TYPE-III 3.
PIBRONECTIN TYPE-III 4.
PIBRONECTIN TYPE-III 4.
PROTEIN-TYROSINE PHOSPHATASE 1
PROTEIN-TYROSINE PHOSPHATASE 2
PHOSPHOCYSTEINE INTERMEDIATE ()
                                                                                                                                                                                                                                                          PHOSPHATASE KAPPA.
EXTRACELLULAR (POTENTIAL)
            N-LINKED (GLCNAC.
                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                      RECEPTOR-TYPE PROTEIN-TYROSINE PHOSPHATASE KAPPA.
                                        POTENTIAL.
                                                      SIMILARITY).
                                                                     PHOSPHOCYSTRINE
                                                                                                                                                                                                    IG-LIKE C2-TYPE
                                                                      INTERMEDIATE
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(POTENTIAL)

1. 2. (BY XE)

SPERFFERE

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CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD SEQUENCE

Query Match Best Local S Matches 129

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SEQUENCE FROM N.A.
STRAIN=MRL-LPR/LPR;
MEDLINE=96140699; PubMe
Kuramochi S., Matsuda S
                                                                                                                                                                                                                                                                                         Q64455;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase eta precursor (BC 3.1.3.48) (R-PTP-eta)
(HPTP beta-like tyrosine phosphatase) (Protein-tyrosine phosphatase)
receptor type J) (Susceptibility to colon cancer-1).
PTPRJ OR BYP OR SCC1.
    "Molecular cloning and characterization of receptor-type tyrosine phosphatase similar FEBS Lett. 378:7-14(1996).
                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity
129; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFEHFSVFLETFHVTQYFTVRVFQIVKXSTGKSQCVKHLQFTXHPDHGTPASADFFIKYV : | : | | | | | | | | | | : ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYQRPSHYIATQGPVHETVYDFWRMVWQEQSACIVMVINLVEVGRVKCYKYWPDDTEVYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FFEGQSASWDVAKKDQNRAKNRYGNIIAYDHSRVIIQPVEDDPSSDYINANYIDIWLYRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DFKVTCVEMEPL---AEYVVRTFTLERRGYNEIREVKQFHFTGWPDHGVPYHATGLLSFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EY----FYIATQGPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FNSGNTL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LMVFLLIKTIWYNVFKLWKGKLIFGNK--MNSENVKPSHHL----SFSDKYELVYPEPL
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415
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         Pfam; PF00041; fn3; 6.

Pfam; PF00102; Y phosphatase; 1.

Pfam; PF00102; Y phosphatase; 1.

PRINTS; PR00700; PRTYPHPHTASE.

SMART; SM00160; FN3; 6.

SMART; SM00194; PTPC; 1.

PROSITE; PS00038; TYR PHOSPHATASE 1; 1.

PROSITE; PS50056; TYR PHOSPHATASE 2; 1.

PROSITE; PS50055; TYR PHOSPHATASE PTP; 1

Signal; Glycoprotein; Transmembrane; Rep
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InterPro; IPR008957; FN III-like.
InterPro; IPR008951; FN III.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000242; Tyr PP.
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-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Expressed in every tissue examined.
-!- SIMILARITY: Contains 1 protein-tyrosine phosphatase dom
-!- SIMILARITY: Contains 6 fibronectin type III domains.
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GO:0007507; P:heart development;
GO:0001570; P:vasculogenesis; IM
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10-OCT-2003 (Rel. 42, Last amnotation update)
Protein-tyrosine phosphatase beta precursor (EC
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01-NOV-1991 (Rel. 20,
01-NOV-1991 (Rel. 20,
10-OCT-2003 (Rel. 42,
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                      TISSUE=Placenta;

MEDLINE=91006018; PubMed=2170109;

Krueger N.X., Streuli M., Saito H.;

"Structural diversity and evolution of human recept
tyrosine phosphatases.";

EMBO J. 9:3241-3252(1990).

EMBO J. 9:3241-3252(1990).
                                                                                                                                                                                                  SEQUENCE FROM N.A. TISSUB=Placenta:
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Mammalia; Eutheria;
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                                          tyrosine + phosphate.
SUBCELIJIAR LOCATION: Type I membrane protein.
SIMILARITY: Contains 1 protein-tyrosine phosphatase
SIMILARITY: Contains 16 fibronectin type III domains
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GO; GO:0005001; F:transmembrane receptor protein tyrosine pho.
GO; GO:0006796; P:phosphate metabolism; TAS.
GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
InterPro; IPR000985; FN III-like.
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Glycoprotein; Transmembrane; Hydrolase; 3:

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C TISSUE-Ridney;
C TISSUE-Ridney;
A Ansorge W., Wirkner U., Mewes H.W., Gassenhuber J., Wiemann P. L Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, ALOSO040; CRB43248.1; -.
R PIR; T08716; T08716.
R HSSP; Q06124; 2SHP.
RHSSP; Q06124; 2SHP.
RGO; G0:0016797; F:hydrolase activity; IEA.
RGO; G0:0014725; F:protein tyrosine phosphatase activity; IEA.
DR GO; G0:006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000342; Tyr_PP.
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Pfam; PP00102; Y_phosphatase; 1.

PRINTS; PR00700; PRTYPHPHTASE;

SMART; SM00194; PTPC; 1.

PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.

PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.

PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9Y406;
01-NOV-1999
01-NOV-1999
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                          DKFZP566K0524.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein
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                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
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9 (TrEMBLrel. 12, Last s
3 (TrEMBLrel. 24, Last a
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Primates;
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Pred. No. 1.9e-163;
0; Mismatches 0;
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Catarrhini; Hominidae;
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R PRINTS; PR00700; PRTYPHPHTASE.

R SMART; SM00194; PTPC; 1.

PROSITE; PS00183; TYR PHOSPHATASE 1; 1.

PROSITE; PS0056; TYR PHOSPHATASE 2; 1.

PROSITE; PS50055; TYR PHOSPHATASE PTP; 1.

PROSITE; PS50055; TYR PHOSPHATASE PTP; 1.

SEQUENCE TO 1

SEQUENCE TO 1.
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                                                                [1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=SKIN;
MEDLINE=96340953; PubMed=8749712;
Medariks W., Schepens J., Baechner D., Rijss J., Zeeuwen P.
Zechner U., Hameister H., Wieringa B.;
"Molecular cloning of a mouse epithelial protein-tyrosine with similarities to submembranous proteins.";

* Call. Biochem. 59:418-430(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q64512 PRELIMINARY; PRT; 2460 AA.
Q64512; Q621494; Q64499;
Q64512; Q62135; Q621494; Q64499;
Q1-NOV-1996 (TIEMBLIFE1 01, Created)
Q1-NOV-1996 (TIEMBLIFE1 01, Last sequence update)
Q1-JUN-2003 (TIEMBLIFE1 24, Last annotation update)
Protein-tyrosine phosphatase, NONRECEPTOR-type, 13 (BC 3.1.3.48)
(Protein-tyrosine phosphatase RIP) (Phosphoprotein phosphatase)
(Protein-tyrosine-phosphatase) (Phosphotyrosine phosphatase) (PTPASE)
                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
MEDLINE=95145716; PubMed=7843407; Chida D., Kume T., Mukouyama Y.,
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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Pred. No. 4.1e-93;
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R GO; GO:0005871; C:kinesin complex; IEA.
R GO; GO:0016787; F:hydrolase activity; IEA.
R GO; GO:0004727; F:hydrolase activity; IEA.
R GO; GO:0004727; F:prenylated protein tyrosine phosphatase act. of GO:0005188; F:struccural molecule activity; IEA.
R GO; GO:0005189; F:struccural molecule activity; IEA.
R GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
R GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
R Interpro; IPR000299; Band 4.1:
R Interpro; IPR000387; TYR phosphatase.
R Interpro; IPR000387; TYR pp.
R Interpro; IPR000387; TYR pp.
R Interpro; IPR000387; TYP pp.
R Pfam; PF00373; Band 4.1; I.
R PRINTS; PR00700; PRTYPHPHTASE.
R SMART; SM00295; B41; 1.
R SMART; SM00295; B41; 1.
R SMART; SM00295; PDZ; 5.
R SMART; SM00218; PTPC; 1.
                                                                                                                                         PROSITE; PS00660; FERM 1; FALSE NEG.
PROSITE; PS00661; FERM 2; FALSE_NEG.
PROSITE; PS50057; FERM 3; 1.
PROSITE; PS50106; PDZ; 5.
PROSITE; PS50106; PDZ; 5.
PROSITE; PS00383; TYR PHOSPHATASE 1; FA
PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
PROSITE; PS50055; TYR PHOSPHATASE PTP; PROSITE; PS50055; TYR PHOSPHATASE PTP.
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"A novel receptor-type protein tyrosine phosphatase with a single catalytic domain is specifically expressed in mouse brain.";
Biochem. J. 305:499-504(1995).

-i- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 = PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1105-2460 FROM N.A.
STRAIN-CB.17 SCID; TISSUE=THYNUS;
MEDLINE=94354845; PubMed=8074693;
MEDLINE=94354845; PubMed=8074693;
"CDNA cloning of a novel protein tyrosine phosphatase with homology cytoskeletal protein 4 land its expression in T-lineage cells.";
Ecchem. Biophys. Res. Commun. 203:479-484(1994).
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EMBL; D83966; BAA11158.1; -.
EMBL; D28529; BAA05885.1; -.
EMBL; Z23059; CAA80594.1; -.
EMBL; Z23059; CAA80594.1; -.
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!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTEY IN KIDNEY ALLESSER EXTENT, IN LUNA, HEART, BRAIN AND TESTIS.

-!- SIMILARITY: CONTAINS A DOMAIN FOUND IN BAND 4.1, EZRIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 2266-2372 FROM N.A. STRAIN=BALB/C; TISSUE=BRAIN; MEDLINE=95134232; PubMed=7832766;
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"Characterization of a protein tyrosine phosphatase (RIP) expressed a very early stage of differentiation in both mouse erythroleukemia a very early stage of differentiation in both mouse erythroleukemia and embryonal carcinoma cells.";
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MGI:103293; Ptpn13.

GO:0005856; C:cytoskeleton; IEA.

GO:0005871; C:kinesin complex; IEA.
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BAND 4.1-LIKE DOMAIN.

PROTEIN-TYROSINE PHOSPHATASE.

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5 APPROXIMATE REPEATS.
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DHR/GLGF REPEAT 2.
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GG; GG:00004725; F:protein tyrosine phosphatase activity; IEA.

RG GG: GG:0000742; P:intracellular signaling cascade; IEA.

RG GG: GG:0000740; P:protein amino acid dephosphorylation; IEA.

RINTEPPO; IPR000399; Band 4:1.

RINTEPPO; IPR000397; TYR phosphatase.

InterPro; IPR000387; TYR phosphatase.

InterPro; IPR000387; TYR phosphatase.

RINTEPPO; IPR000387; TYR phosphatase.

RINTEPPO; IPR000387; TYR phosphatase.

R Pfam; PF00373; Band 4:1 I.

R Pfam; PF00373; Band 4:1 I.

R Pfam; PF00102; Y phosphatase; 1.

PR Pfam; PF00102; Y phosphatase; 1.

PR Pfam; PF00102; Y phosphatase; 1.

R Pfam; PF00102; Y phosphatase; 1.

R PRINTS; PR00593; BAND4:

R PRINTS; PR00593; BAND4:

R PRINTS; PR00700; PRTYPHPHTASE.

R SMART; SM00192; PNTC; 1.

R SMART; SM00192; PNTC; 1.

R SMART; SM00192; PTC; 1.

R SMART; SM00192; PTC; 1.

R SMART; SM00192; PTC; 1.

R PROSITE; PS00660; PERM 1; FALSE_NEG.

PROSITE; PS00661; PERM 3; 1.

R PROSITE; PS00057; FERM 3; 1.

R PROSITE; PS00056; TYR PHOSPHATASE 1; FALSE_NEG.

PROSITE; PS00056; TYR PHOSPHATASE 7; 1.
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PS00661; FERM_2; FALSE_NEG.
PS0057; FERM_3; 1.1.
PS50057; FERM_3; 1.1.
PS500106; PDZ; 5.
PS500106; PERM_3; TYR_PHOSPHATASE_1; FALSE_NEG.
PS500106; PERM_3; PPD; 1.
PS500106; PERM_3; PPDSPHATASE_PTD; 1.
PS500106; PERM_3; PPDSPHATASE_PTD; 1.
PS500106; PERM_3; PPDSPHATASE_PTD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKMNSENV------KPSHHLSFSDKYELVYPE--PLESDTDETVWDVSDRSLRNRW
                                                                                                                                                                                               WQMVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVR
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                                                                                                                                                                                                                                                                                     AMTLEDIQTGEVRHVSHLNFTAWPDHDTPSQPDDLLTFISYMRHVHRSGPIITHCSAGIG
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    (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
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35.0%; Pred. No. 3.3e-41;
tive 70; Mismatches 144;
      12,
12,
25,
      Last sequence update)
Last annotation update)
                                                  Created)
                                                                                           PRT;
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Query Match
Best Local Sim
Matches 146;
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InterPro; IPR000299; Band_4.1.
InterPro; IPR000299; Band_4.1.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; TYr_PP.
Pfam; PF000373; Band_41; 1.
Pfam; PF000373; Band_41; 1.
Pfam; PF00102; Y_phosphatase; 1.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR0010595; BAND41.
PRINTS; PR0010595; BAND41.
SMART; SM00295; B41; 1.
SMART; SM00295; B41; 1.
SMART; SM00296; PDZ; 1.
SMART; SM00296; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -|- SIMILARITY: CONTAINS 1:
EMBL; AF106702; AAD22773.1;
HSSP; P29350; 1GWZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Park K.W., Lee B.J., Lee S.H., Lee J.E., Choi E.Y., Kim B.J., Hwang R., Park K.A., Baik J.H.; Hwang R. cloning and characterization of a protein tyrosine phosphatase enriched in testis, a putative murine homologue of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa;
Mammalia, Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00660; FERM 1; 1.

PROSITE; PS00661; FERM 2; 1.

PROSITE; PS50067; FERM 3; 1.

PROSITE; PS50106; PDZ; 1.

PROSITE; PS50108; TYR PHOSPHATASE 1; 1.

PROSITE; PS50056; TYR_PHOSPHATASE_PTP; 1.

PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20510023; PubMed=11054567;
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SEQUENCE
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            309 YSYWPISLKEPLEFEHFSVFLETFHVTQ---YFTVRVFQIVKKSTGKSQCVKHLQFTKWP
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                                                                                                                                 GLITGTVLAQFDQLYRKKPGWTMSCAKLPQNISKNRYRDISPYDATRVLLKGNEDYINAN
                                                                                                                                                                                                                                                                                                                                                                            IPHDNLVLIKMKPDENGRFGFNVKGGYDQKMPVIVSRVAPGTPADLCVPRLNEGDQVVLI
                                                   YINMEIPSSSIINQ-----YIACQGPLPHTCKDFWQMIWBQGSSMVVMLTTQVERGRVKC
                                                                                                                                                             EL---DIIREFLELBOMTLPDDFNSGNTLONRDXNRYRDILPYDSTRVPLGKNKDYINAS
                                                                                                                                                                                                                                                       AGPSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQKKE 198
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                                                                                                                                                                                                                                                                                                NGRDIAEHTH----DQVVLFIKASCEKHSGELVLLVRPNAVYDVVEEKLE-------
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Rodentia;
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%; Pred. No. 3.1
83; Mismatches
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Mismatches 177;
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Best Local S
Matches 102
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PRINTS, PROOTOO, PRITTPHHTASE.

SMART; SMO0194; PTPC; 1.

SMART; SMO0404; PTPC; motif; 1.

PROSITS; PS00015; MITOCH_CARRIER; 1.

PROSITS; PS000383; TYR PHOSPHATASE 1; 1.

PROSITS; PS500385; TYR PHOSPHATASE 2; 1.

PROSITS; PS50055; TYR_PHOSPHATASE_PTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSN4S3 PRELIMINARY; PRT; 292 AA.
QSN4S3;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC033716; AAH33716.1; ...
GO; GO:0005743; C:mitochondrial inner membrane; IEA.
GO; GO:0005488; F:binding; IEA.
GO; GO:0005488; F:binding; IEA.
GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR003995; PTPC_motif.
InterPro; IPR003997; TYT_PP.
InterPro; IPR003997; TYT_PP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
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XY.
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                                                                                                     HCSAGIGRTGVLVTMETAMCLTERNLPIYPLDIVRKMRDQRAMMVQTSSQYKFVCEAILR
                                                                                                                                                                                                           IAYVSREMLVTNTQTGEEHTVTHLQYVAWPDHGVPDDSSDFLEFVNYVRSLRVDSEPVLV
                                                                                                                                                                                                                                                                                                                                            TIEDPWOMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEH--PSVFLETPHVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        QNRDKNRYRDILFYDSTRVFLGKNKDYINASYI-----RIVNHEEEYFYIATQGFLFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLDIVRTMRDQRAMMIQTPSQYRFVCEAILKVYB
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                                                                                                                                                  HCSAGVGRTGVFICVDVVFSAIEKNYSEDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLE
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Pred. No. ie-30;
38; Mismatches
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InterPro; IPR003961; FN III.
InterPro; IPR003957; FN III-like.
InterPro; IPR009957; FN III-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig-C2.
InterPro; IPR003987; TYR_phosphatase.
InterPro; IPR000242; Tyr_PP.
Pfam; PF00041; fn3; 8.
Pfam; PF000041; ig; 3.
Pfam; PF00102; Y phosphatase; 2.
PRINTS; PR00106, PRTYPBEIII.
PRINTS; PR00700, PRTYPBHTASE.
PRINTS; PR00700, PRTYPBHTASE.
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044328;
01-JUN-1998
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SMART; SM00108; FN3; 7.

SMART; SM00108; FTPC; 2.

SMART; SM00104; PTPC; 2.

PROSITE; PS50835; IG LIKE; 3.

PROSITE; PS50835; TYR PHOSPHATASE 1; 2.

PROSITE; PS50056; TYR PHOSPHATASE 2; 2.

PROSITE; PS50056; TYR PHOSPHATASE 2: 2.

PROSITE; PS50056; TYR PHOSPHATASE 2: 2.

PROSITE; PS50056; TYR PHOSPHATASE 2: 2.

Hydrolase; Immunoglobulin domain; Repeat.

Hydrolase; Immunoglobulin domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gershon T.R., Baker M.W., Nitabach M., Wu P., Macagno E.R.;
"Two receptor tyrosine phosphatases of the LAR family are ex
the developing leech by specific central neurons as well as
peripheral neurons, muscles, and other cells.";
J. Neurosci. 18:2991-3002(1998).
EMBL; AP017083; AAB91460.1;
EMBL; AP017083; AAB91460.1;
PIR; T30938; T30938.
HSSP; P28827; IRPM.
GO; GO:00016787; F:hydrolase activity; IEA.
GO; GO:00016787; P:protein amino acid dephosphorylation; IEA.
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01-JUN-1998 (TrEMBLrel. 06, La
01-OCT-2003 (TrEMBLrel. 25, La
Receptor tyrosine phosphatase.
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ORCGMIQTKEQYQFCYBIVLEVL
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                                             DFIGOTHKTKEOFGOEGPIAVHCSAGVGRTGVFITLSIVLERMRFEGAVDVFQTVNVLRT
                                                                                                         SARYQYEYVDPLAEYNMEQYI-LREEKVTDARDGQSRTMRQFQLTDWEBQGVPSTGDGFI
                                                                                                                                                                                                                                 EFKKLSSGKTSLSSFASANLSCNKQKNRLVNVLPYETTRVCLQPIRGVDGSDYINASFID
                                                                                                                                                                                                                                                             EFLEGEO-WILPODFNSGNTLQNRDKNRYRDILFYDSTRYPLG----KNKDYINASYIR
                                                                          KYVRYVRKSH----ITGPLLVHCSAGVGRTGVFICVDVVFSAIBKNYSFDIMNIVTQMRK
                                                                                                                                     PLEFEHFSVF-LETFHVTQVFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFI
                                                                                                                                                                     --GYRYRRAYIATQGPLPDTVEDFWRALWESNCNIIVMLTKLREMGREMCHQYWP--SER
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40.3%; Pred. No. 2.30
tive 46; Mismatches
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Q9IAI8;
01-OCT-2000
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Q9JIJB;
Q9JIJB;
01-OCT-2000
01-OCT-2000
01-JUN-2003
PTP36-B isofe
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Mech. Dev. 92:291.294(2001).
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Receptor protein tyrosine phosphatase CRYP-alpha (Fragment)
Xenopus laevis (African clawed frog)
Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000242; Tyr PP.
Pfam; PF00102; Y phosphatase; 2.
PRINTS; PR00700; PTYPHPHTASE.
SMART; SM00194; PTPC; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
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PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
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Best Local Sim
Matches 139;
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R GG; GG:0005856; C:cytoskeleton; IEA.

R GG; GG:0004725; F:pyctcin tyrosine phosphatase activity; IEA.

R GG; GG:0004725; F:pyctcin amino acid dephosphorylation; IEA.

R InterPro; IPR000299; Band 4:1.

R InterPro; IPR000242; Tyr PP.

R InterPro; IPR000242; Tyr PP.

R Pfam; PF00173; Band 4:1.

R Pfam; PF00173; Band 4:1.

R Pfam; PF00173; Band 4:1.

R PFINYS; PR00935; BAND4:

R PRINYS; PR00935; BAND4:

R PRINYS; PR00935; BAND4:

R PRINYS; PR00935; BAND4:

R PROSITE; PS00661; PERM 1; 1.

R PROSITE; PS00661; PERM 2; 1.

R PROSITE; PS00661; PERM 3; 1.

R PROSITE; PS00661; PERM 3; 1.

R PROSITE; PS0056; TYR PHOSPHATASE 1; 1.

R PROSITE; PS0056; TYR PHOSPHATASE 2; 1.

R PROSITE; PS0055; TYR PHOSPHATASE 2; 1.

R PROSITE; PS0056; TYR PHOSPHATASE 2; 1.
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Aoyama K., Matsuda T., Aoki N.;
"Characterization of newly identified four isoforms
cytosolic protein tyrosine phosphatase PTP36.";
Biochem. Biophys. Res. Commun. 266:523-531(1999).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
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Pred. No. 7.9
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  Q90YJ4;
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Q9IBA0;
01-OCT-2000
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(SSP; P18052; 1YFO.

30; GO:0016787; F:hydrolase activity; IEA.

30; GO:0016787; F:protein tyrosine phosphatase activity; IEA.

30; GO:0006470; P:protein amino acid dephosphorylation; IEA.

GO: GO:001877; Tyr phosphatase.

InterPro; IPR001837; Tyr phosphatase.

Pfam; PF00102; Y phosphatase; 2.

PRINTS; PR00700; PRTYPHPHTASE.

PRINTS; PR00700; PRTYPHPHTASE.
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GO; GC
GO; GC
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Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
"Protein tyrosine phosphatases from amphioxus,
divergence of tissue-specific isoform genes in
vertebrates.";
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PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
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Elastryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii, Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.
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(TrEMBLrel. 15, Last sequence up
(TrEMBLrel. 24, Last annotation
                                                                                             PRELIMINARY;
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Pred. No. 6.1e-30;
Prematches 90;
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Best Local S
Matches 110
                                                                     Potamotrygon motoro (South American freshwater stingray).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.
                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2003 (TrEMBLrel. 24,
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RYPTPR2AB.
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Prints; PR00700; PRITYPHPHTASE.
SMART; SM00194; PTPC; 2.
PR0SITE; PS00383; TYR PHOSPHATASE 1; 1.
PROSITE; PS50055; TYR PHOSPHATASE 2; 2.
PROSITE; PS50055; TYR PHOSPHATASE PTP;
                                             NCBI_TaxID=86373;
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EMBL; AJ311886; CAC44759.1; -
ZFIN; ZDB-GENB-020107-3; ptprs.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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Brachydanio rerio (Zebrafish) (Danio rerio).
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GO; GO:0004725; F:protein tyrosine ph
GO; GO:0006470; P:protein amino acid
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den Hertog J.;
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R HSSP; P18052; 1YPO.

R GO; GO:0016787; F:hydrolase activity; IEA.

R GO; GO:0016787; F:protein tyrosine phosphatase activity; IEA.

R GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

R GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

R InterPro; IFR000387; TYR Pp.

R InterPro; IFR000242; TYR Pp.

R Pfam; PF00102; Y phosphatase; 2.

PFAINTS; PR00700; PRTYPHPHTASS.

PRINTS; PR00700; PRTYPHPHTASS.

PROSITE; PS00383; TYR PHOSPHATASE 1; 2.

PROSITE; PS00383; TYR PHOSPHATASE 2; 2.

PROSITE; PS00383; TYR PHOSPHATASE 7; 2.
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Best Local Similarity
Matches 108; Conserv
TISSUE=Embryo;

MEDLINE=94122757; PubMed=8293038;

Rowley R., Lee J.M., Corbeil H.B., Charbonneau R., and the control of the control of the control of the control of a brain-specific species related identification of a brain-specific species related (Cell Mol Biol Res. 39:203-219(1993).

EMBL; 127625; PARA9015.1; -.

HSSP; P18052; 17F0.

GO; GO:0016787; F:hydrolase activity; IEA.
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Q90947;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLel. 24, Last annotation update)
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J. Mol. Evol.
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                                                                                                                                                                                                                                                                                                                                                                                                         Phosphotyrosyl phosphatase.
Gallus gallus (Chicken)
Eukaryota, Metazoa, Chordat
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                  Archosauria;
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4; BAA95191.1; -.
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53885
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Neognathae; Galliformes; Phasianidae; Phasiani
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pred. No. 8.7e-30;
pred. rohes 91;
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related to
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the early evolution
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RESULT 14

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DT PTPSI

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PTPsigma-(brain) prec PTPSIGMA. Homo sapiens (Human)

Bukaryota; Metazoa; Mammalia; Butheria; NCBI\_TaxID=9606;

Chordata; Primates;

Craniata; Vertebrata; Buteleostomi; Catarrhini; Hominidae; Homo.

Endo N., Rutled "Human protein inhibition by b J. Bone Miner.

'E FROM N.A.
, Rutledge S.J., Opas E.B., Voger A.
protein tyrosine phosphatase-sigma:
tion by biophosphanates.";
- winar. Res. 0:0-0(1995).

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splicing Schmidt

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SEQUENCE

Q9UM81; Q9UM81; 01-MAY-2000 01-MAY-2000 01-OCT-2003

(TremBirel.) (TremBirel.) (TremBirel.)

EMBLrel. 13, EMBLrel. 13, EMBLrel. 25, ) precursor.

Last sequence update)
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Best Local S
Matches 141
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GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_Pr
Fiam; PF00102; Y_phosphatase; 2.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00194; PTPC; 2.
SMART; SM00194; PTPC; 2.
PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
PROSITE; PS00383; TYR_PHOSPHATASE 2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE 7]; 2.
PROSITE; PS50055; TYR_PHOSPHATASE 7]; 2.
PHOGROLASE.
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FLKHIRTORNYLVQTEBQYIFIHDALVEAI
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                                                                          SADFFIXYVRYGKS-----HITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMN
                                                                                                                               LEFEHFSVFLETFHVTQVFTVRVFQI----VXXSTGK----SQCVXHLQFTXWPDHGTPA
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                 IVTQMRKQRCGMIQTKEQYQFCYBIVLEVL
                                                      --BYTLPVLTFVRKASHAKRHAVGPIVVHCSAGVGRTGTYVVLDSMLQQIQHEGTVNIFG
                                                                                                              -BYGNFLVTQKSVHVLAYYTVRNFTLRWTKIKKGSQKGRSSGRVVTQYHYTQWPDMGVP-
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BGO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

BGO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

BR InterPro; IPR003962; FmIII subd.

BR InterPro; IPR003957; FMIII-like.

BR InterPro; IPR003957; FMIII-like.

BR InterPro; IPR003957; FMIII-like.

BR InterPro; IPR00387; TYM_Plike.

BR InterPro; IPR00387; TYM_phosphatase.

BR InterPro; IPR000387; TYM_PP.

BR InterPro; PP00041; Fn3; 4.

BR Pfam; PP00047; Lybosphatase; 2.

BR Pfam; PP00041; FNTYPPIIII.

BR PRINTS; PR00014; FNTYPPIIII.

BR PRINTS; PR00014; FNTYPPIIII.

BR PRINTS; SM00009; FN3; 4.

BR SMART; SM00109; FN3; 4.

BR SMART; SM00109; IGC2; 2.

BR SMART; SM00109; IGC2; 2.
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Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                   Q8R169;
Q8R169;
Q1-JUN-2002
01-JUN-2002
01-JUN-2003
Strausberg R.;
Submitted (MAR-2002) to the
EMBL; BC025145; AAH25145.1;
PIR; S40282; S40282.
GO; GO:0016787; F:hydrolase
                                                                                                                                                                                                                                             Hypothetical protein.
Mus musculus (Mouse).
Eukaryota, Metazoa; Ch
Mammalia; Butheria; Ro
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PROSITE; PS50383; TYR PHOSPHATASE 1; 2.
PROSITE; PS50056; TYR PHOSPHATASE 2; 2.
PROSITE; PS50055; TYR PHOSPHATASE PTD; 2.
PROSITE; PS50055; TYR PHOSPHATASE PTD; 2.
PHOSPHATASE PTD; 2.
                                                                                                                                         TISSUE=Kidney;
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                   NCBI_TaxID=10090;
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HSSP; P18052; 1YFO.
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Rodentia;
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     activity;
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GO; GO:006470; P:protein amino acid dephosphorylation; IEA.
Interpro; IPR000387; TYR phosphatase.
R Interpro; IPR000242; Tyr PP.
R Pfam; PF00102; Y phosphatase; 2.
R PFINTS; PR00700; PRTYPHPHTASE.
R RRINTS; PR00700; PRTYPHPHTASE.
R SMART; SM00194; PTPC; 2.
R PROSITE; PS00383; TYR PHOSPHATASE 1; 2.
R PROSITE; PS00383; TYR PHOSPHATASE 2; 2.
R PROSITE; PS00383; TYR PHOSPHATASE 7; 2.
R PROSITE; PS00383; TYR PHOSPHATASE 7; 2.
R PROSITE; PS00383; TYR PHOSPHATASE 7; 2.
R PROSITE; PS00383; TYR PHOSPHATASE 7; 2.
R PROSITE; PS00383; TYR PHOSPHATASE 7; 2.
R PROSITE; PS00383; TYR PHOSPHATASE 7; 2.
R PROSITE; PS00383; TYR PHOSPHATASE 7TP; 2.
R PROSITE; PS00383; TYR PHOSPHATASE 7TP; 2.
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Best Local
  716
                                      431
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                                                                                                                                                                                                                                                                                                                      207 LELEQMTLPDD-----FNSGNTLQNRDKXRYRDILPYDSTRVPLG-----KNKDYINAS
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                    MRKQRCGMIQTKEQYQFCYEIVLEVL 456
                                                                                                                                                                    LKEPLEFEHFSVF-LETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTXWPDHGTPASAD
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LRTQRPAMVQTBDQYQFCYRAALSYL
                                                                          GFIDFIGQVHKTKEQFGQDGPISVHCSAGVGRTGVFITLSIVLERMRYEGVVDIFQTVKM
                                                                                                            PFIKYVRYVRKSH----ITGPLLVHCSAGVGRTGVFICVDVVFSAIBKNYSFDIMNIVTQ
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Pred. No. 2.3e-29;
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Search completed: June 18, 2004, 19:40:03
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Perfect score:
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463
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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383 362 299 299 1199 1199 1199 1155 1155 1155	Score 463
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## ALIGNMENTS

PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease;

Mouse PTP05 isoform #1.

AAW89250;

AAW89250 standard; protein; 463 AA.

10-MAR-1999

(first entry)

Parkinson's disease; Huntington's disease.

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RESULT 1
AAW89250
ID AAW8
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20-MAY-1997;
11-JUN-1997;
11-JUN-1997;
18-JUN-1997;
                                                                                                                                                                                                       New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.
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N-PSDB; AAV81745.
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The present invention describes isolated, acids encoding PTP04, SAD, PTP05, PTP10, present sequence represents mouse PTP05.

ALK-7, are protein tyrosine phosphatases

, enriched or purified nucleic ALP and ALK-7 proteins. The The above proteins, other than (PTPs) and are used to identify

Claim 2;

Page 157-158; 193pp; English.

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                                                                                                                                                                                                                                PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphom neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease.
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N-PSDB; AAV81744.
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                                                                                                                                             The present invention describes isolated, enriched or purified nucleic CC acids encoding PTP04, SAD, PTPD5, PTPD19, ALP and ALK-7 proteins. The present sequence represents mouse PTP05. The above proteins, other than CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify CC substances that modulate their activity (i.e. agonists and antagonists, CC including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways CC that involve the proteins, particularly cancer (e.g. leukaemia and CC lymphoma), while modulators of ALK-7 (which is a type I receptor CC serine/threonine kinase) are used to promote neuronal survival, CC diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences, to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
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The present invention describes isolated, enriched or purified nuclearids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their actions. (i.e. agonists and antagonists, including NBP) in vivo or in vitro.

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Example 14;

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Page 108; 193pp; English

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20-MAY-1997;
11-JUN-1997;
11-JUN-1997;
18-JUN-1997;
23-OCT-1997;
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                                                                                                                                                                                                                New nucleic acid encoding specific protein for identifying specific modulators for tre cancer and neurodegenerative disease.
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The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly
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The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal

New nucleic acid encoding specific protein for identifying specific modulators for tre cancer and neurodegenerative disease.

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Example 14;

Page 108; 193pp; English.

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11-JUN-1997;
11-JUN-1997;
18-JUN-1997;
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20-MAY-1997;
11-JUN-1997;
                     The present invention describes isolated, enriched or purified nucleic acids encoding PT004, SAD, PT005, PT010, ALP and ALK-7 proteins. The present sequence represents rat PT010. The above proteins, other than A-7, are protein tyrosthe phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor
                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding specific protein tyrosine phosphatases for identifying specific modulators for treatment and prevention cancer and neurodegenerative disease.
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19-DEC-2001; 2001US-0343007P.
21-DEC-2001; 2001US-034346P.
04-PEB-2002; 2002US-0357675P.
15-FEB-2002; 2002US-0357675P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer; psoriasis; thromobocytopaenia; developmental disorder; Reiter's syndrome; renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease; neurological disorder; Parkinson's disease; policpsy; glomerulonephritis; autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome; acquired immune deficiency syndrome; immunosuppressive; Crohn's disease; nootropic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus; allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome; osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological; gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.
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The invention relates to an isolated polypeptide, which and phosphatase (KPP). KPP agonists and antagonists are

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kinase

New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disole. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis cancer or hepatitis.

disorders

Claim 1;

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242; 282pp; English.

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Chiflammatory disorders (e.g. AlDS; acquired immune deficiency syndrome, callergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's callergies, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, contact dermatitis, Crohn's couput, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome, callergies, osteoparthritis, osteoporosis, pancreatitis, syndrome, cultiple sclerosis, osteoparthritis, osteoporosis, pancreatitis, retter's syndrome, rheumatoid arrhritis, Sjogren's syndrome, uveitis), or viral, conterial fungal, parasitic, protozoan or helminthic infections. The KPP concerning the effects of exogenous compounds on the compounds on the compounds on the constant of nucleic acids and kinases and phosphatases. KPP gene is useful in gene therapy and for creating transgenic animals to model human constant of the present sequence is human KPP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
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                                                                                                                                                                                                                 New human tyrosine phosphatase polypeptide, the regulation of which useful for treating obesity, diabetes, cardiovascular or central new system disorder, chronic obstructive pulmonary disease and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; tyrosine phosphatase; obesity; diabetes; Parkinson's disease; central nervous system disorder; CNS; cardiovascular disorder; stroke; chronic obstructive pulmonary disease; cancer; multiple solerosis; Alzheimer's disease; Huntington's disease; congestive heart failure;
                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-2000; 2000US-0252912P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human tyrosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosing, treating or preventing disorders associated with aberrant expression of KPP, particularly cell proliferative disorders (e.g. arteriosclerosis, atheroselerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FARB )
                                                                                                                                                                                                                                                                                                                                                  2002-575236/61.
)B; ABK89178.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KORYRDILPYDSTRVPLGK 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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J. 1.8e-10;
O;
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                                            dysfunction related disease, preferably the above mentioned diseases. The invention is useful for treating the above mentioned disorders, where the CNS disorder is selected from Parkinson's disease, multiple sclerosis, stroke, Alzheimer's disease, and Huntington's disease, and the cardiovascular disorder is selected from congestive heart failure and myocardial infarction. The molecules of the invention are useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to disease and abnormalities related to the presence of mutations in the polymucleotide coding the polymeptide of the invention. The present amino acid sequence represents the human tyrosine phosphatase protein #1 of the invention. This sequence is encoded by the human tyrosine phosphatase gene located on chromosome 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                   chronic obstructive
                                                                                                                                                                                                                                                                                                                                                                                                                 onic obstructive pulmonary disease, cardiovascular disorder or invention is useful for treating a human tyrosine phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorder or
                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer.
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            S
                            Matches
                                   Best
                                         Query Match
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164
                                   Similarity
KNRYRDILPYDSTRVPLGK
            KNRYRDILPYDSTRVPLGK
                            Conservative
                                  4.1%;
                           ,
0
182
             247
                                  Score 19;
Pred. No.
                            Mismatches
                                   DB 5; L
2.7e-10;
                            0,
                                         Length 398
                             Indels
                            0,
                            Gaps
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Sequence 398

ΑA,

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antiarthritic; antipsoriatic; antiarteriosclerotic; antiinflammatory; vulnerary; gynaecological; antiangiogenic; hyperproliferative disease; autoimmune disease; diabetes mellitus; multiple sclerosis; rheumatoid arthritis; psoriasis; atherosclerosis; inflammation; scarring;
                                                                                                                                                                                                                                                                                                                      immunosuppressive; antidiabetic; neuroprotective; antirheumatiantiarthritic; antipsoriatic; antiarteriosclerotic; antiinflan
                                                                                                                                                                                                                                                                                                                                          cancer associated phosphatase; enzyme; human; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                              Human DKFZP566K0524 protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                     ADD89795 standard; protein; 398
                                                                                                                                                                                                                                                                                     endometriosis;
                                                                                                                                                                                                                                                                                                                                                                                 (first
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                                                                                                                                                                                                                                                                                                                                                               NO:10
                                                                                                                                                                                                                                                                                                                                            cytostatic;
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Homo sapiens
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WO2003083102-A2

09-OCT-2003

19-MAR-2003; 2003WO-CA000393.

28-MAR-2002; 2002US-0368859P

(KINE-) KINETEK PHARM INC

N-PSDB; 2003-902934/82. ADD89794

New nucleic acids encoding cancer associated phosphatases, ustargets for screening pharmaceutical agents that inhibit the tumor cells, or for diagnosing and treating cancer, inflammateur. autoimmune disease. inflammation useful e growth of tion or

Claim <u>بر</u> SEQ IJ ö 10; 63pp; English.

or central nervous and cancer.

nucleic acid. Also described: (1) a method of screening for biologically active agents that modulate a cancer associated phosphatase function; (2) a method for the diagnosis of cancer; (3) a method for inhibiting the growth of a cancer cell; (4) methods of screening for targets.

The

Claim

25;

Fig

2

145pp; English

for modulating

present invention relates to a new human tyrosine phosphatase ypeptide. The invention is useful for the preparation of a medicament modulating the activity of human tyrosine phosphatase in a disease h as obesity, diabetes, a central nervous system (CNS) disorder,

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CC associated phosphatase, where the targets are associated with signal C transduction in cancer cells; (5) a compound (C) for the treatment of a tumour; (6) a composition for the treatment of a tumour; (6) a composition for the treatment of a tumour; (6) a composition for the treatment of a tumour; (6) a composition for the treatment of a tumour; and CC pharmaceutical carrier and (C); (7) methods for treating a tumour; and composition and the present invention has cytostatic, immunosuppressive, antidiabetic, neuroprotective, antirheumatic, antiarthritic, year contrological and antiangiogenic activities. The cancer associated phosphatases and nucleic acids encoding the proteins are useful for cyisualiaing tumours in patients or diagnosing and treating cancer, e.g. compositions are useful for cyisualiaing tumours in patients or diagnosing and treating cancer, e.g. compositions and archive diseases, compareas, lung, ovarian, liver or colon cancer. The polypeptides and concernate autoimmune disease, diabetes mellitus, multiple sclerosis, concentrated arthritis, psoriasis, atherosclerosis, inflammation, scarring, condometriosis or angiogenesis, determining the effectiveness of drugs, concernation patient prognosis, or as targets for screening pharmaceutical agence represents the human cancer associated phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                     11-DEC-2001;
14-MAR-2002;
14-MAR-2002;
12-APR-2002;
12-APR-2002;
22-APR-2002;
24-APR-2002;
                                          Μa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              novel gene;
                                                                                                                                  (HYSE-)
                                                                                                                                                                                                                                                                                                                          10-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                              10-DEC-2002; 2002WO-US039555
                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003054152-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE09123 standard; protein;
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                                                               <u>*</u>, ',
2003-569235/53
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                                          Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
19; Conserv
                                                                                                                               HYSEQ INC
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                                     Asundi V, Goodri
Xue AJ, Wehrman '
ng D, Chen R, Xu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNRYRDILPYDSTRVPLGK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           marker;
                                                                                                                                                                       2001US-0339453P.
2002US-0365091P.
2002US-0365384P.
2002US-0372381P.
2002US-0372615P.
2002US-00128558.
2002US-00128569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel
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llarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; tissue marker; molecular weight marker;
genetic disorder; contig.
                                     Goodrich RW,
Wehrman T, Wen
n R, Xu C, Bc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig polypeptide sequence #189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               %; Score 19; DB
%; Pred. No. 2.7
0; Mismatches
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                                        RW, Ren F, Zha
Weng G, Zhou I
, Boyle BJ;
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2.7e-10;
0;
                                                                                Zhang
                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 398;
                                                             J, Zhao QA,
Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                             Wang
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New polynucleotides, analysis, characteri

characterization

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for expressing or therapeutic u

use, or as markers for

for tissues

for

New human kinases and phosphatases and polynucleotides, useful diagnosing, treating or preventing autoimmune or inflammatory (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthr:

disorders

N-PSDB; AAD57368

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence was used in the exemplification of the invention.
                                                                                                                       Kable AB,
Hafalia A
                                                                                                                                                                                                                                                                                                                                                                                 Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis; atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer; psoriasis; thromobocytopaenia; developmental disorder; Reiter's syndrome; renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease; neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis; autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome; acquired immune deficiency syndrome; immunosuppressive; Crohn's disease; nootropic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus; allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome; osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological; gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.
                                                                                                                                                                                        07-DEC-2001; 2001US-0340235P.
19-DEC-2001; 2001US-0343007P.
21-DEC-2001; 2001US-0343546P.
04-FEB-2002; 2002US-0354388P.
15-FEB-2002; 2002US-0357675P.
                                                                                                                                                                                                                                                                         06-DEC-2002; 2002WO-US039126
                                                                                                                                                                                                                                                                                                     19-JUN-2003
                                                                                                            Baughn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human kinase and phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE37996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 2667; 1177pp; English.
                                                                                                                                                                (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in which the corresponding protein is preferentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                   2003-532894/50.
                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                          <u>₹</u>
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                                                                                                                       AJA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNRYRDILPYDSTRVPLGK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 AA;
                                                                                              E
6
                                                                                                                                    Chien D,
                                                                             Thien D, Wilson AD, Swarn, Jin r, Emerling BM, Ramkumar J, Jin r, Khare R, Lehr-Mason PM, Khare R, Ww. Zebarjadian Y,
                                                                                                            Chawla NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.1%;
larity 100.0%;
Conservative
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2.8e-10;
                                                                                            e P
                                                                                                                                      Gorvad AE;
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                                                                                                          Griffin
Lee S,
                                                                                                            JA, Marquis JP;
Hawkins PR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; protein phosphatase; PP-4; immune system disorder; AIDS; allergy; neurological disorder; developmental disorder, Alzheimer's disease; cell proliferative disorder; Huntington's disease; arteriosclerosis; renal tubular acidosis; gonadal dysgenesis; cancer; adenocarcinoma; leukaemia; transgenic animal; gene therapy.
    16-JUN-2000; 2000US-0212447P.
22-JUN-2000; 2000US-0213746P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                14-JUN-2001; 2001WO-US019442.
                                                                                                                                                                                                                                                                          WO200196546-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183. .411
                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Tyr_phosphatase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .388
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                                                                                                                                                                                                                                                                                                                                                          Transmembrane domain
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; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specific protein phosphatase active
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Crespiratory distress syndrome, allergies, amyloidosis, anaemia, asthma, catherosclerosis, Crohn's disease, aropic dermatitis, diabetes mallitus, catherosclerosis, Crohn's disease, aropic dermatitis, diabetes mallitus, cemphysema, Goodpasture's syndrome, gout, Graves' disease, multiple constending mayasthenia gravis, myocardial or pericardial inflammation, costeoparosis, myasthenia gravis, myocardial or pericardial inflammation, costeoparosis, pancreatitis, psoriasis, Reiter's syndrome, creaming and other developmental disorders include Alzheimer's disease, mental creatration and other developmental disorders of central nervous system companies, specifical disorders include a palsy, periodic paralysis, mental creatration and other developmental disorders of central nervous system companies, as bown's syndrome, cerebral palsy, periodic paralysis, mental creatrated disorders include and schizophrenic disorders, seasonal caffective disorders include e.g. actinic paralysis, buchenne and cerebral popmental disorders include e.g. actinic keratosis, Duchenne and cerebral popmental disorders include e.g. actinic keratosis, arteriosclerosis, atherosclerosis, burstitis, cirrhosis, hepatitis, portiasis and cancer circluding adenocarcinoma, leukaemia. The polypeptide and polynucleotide care further useful for analysing proteome of a tissue or a cell type, for screening an agonist, anaemia, animale of a tissue or actil to model humanised animals (pigs) or transgenic animals (mice or rate) to model humanised animals for or remerating a transcrint image of a tissue or cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hafalia A, Ke
Ramkumar J, R
Tribouley CM,
Sequence 420 AA;
                                           human disease, for generating a transcript image of a tissue or cell
type, which represents the global pattern of gene expression by a
particular tissue or cell type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prevention of immune system disorders, neurological disorders, developmental disorders and cell proliferative disorders. Examples immune system disorders include acquired immune deficiency syndrome (AIDS), severe combined immunodeficiency disease (SCID), adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is human protein phosphatase (PP)-4. PP polynucleotide and polypeptide are useful in the diagnosis, tr prevention of immune system disorders, neurological disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptide, useful for diagnosing, treating or preventing disorders of growth and development, immune system, neurological proliferation diseases, comprises cancer protein phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-2000; 2000US-0215210P.
06-JUL-2000; 2000US-0216529P.
12-JUL-2000; 2000US-0218080P.
21-JUL-2000; 2000US-0220117P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 105-106; 116pp; English
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Lee EA,
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Best Local
Novel protein (useful for identifying genetic
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                                                                                 ADE08106
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                                                                                                                                                                                                           l Similarity
19; Conserv
                                                                                 standard; protein; 508 AA
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100.0%; Pred. No. 2.
tive 0; Mismatches
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2.8e-10;
   disorders)
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Best Local
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11-DEC-2001;
14-MAR-2002;
14-MAR-2002;
14-MAR-2002;
12-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein of the invention.
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22-APR-2002;
24-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
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               W0200175067-A2
                                          Homo sapiens
                                                                                                             Novel human diagnostic protein #6033.
                                                                                                                                            13-FEB-2002
                                                                                                                                                                       ABG06042;
                                                                                                                                                                                                   ABG06042 standard; protein; 561 AA
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 1172; 1177pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ng YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, 
Ssh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, 
Y, Wang D, Chen R, Xu C, Boyle BJ;
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DB; ADE07195.
                                                                    supplement;
                                                                                                                                                                                                                                                                       229 KNRYRDILÞYDSTRVÞLGK 247
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274 KNRYRDILÞYDSTRVÞLGK 292
                                                                                                                                                                                                                                                                                                                                19;
                                                                    chromosome mapping; gene mapping; gene therapy; forensic;
upplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 2002US-0365384P.
; 2002US-0372381P.
; 2002US-0372615P.
; 2002US-00128558.
; 2002US-0376045P.
                                                                                                                                                                                                                                                                                                                                Conservative
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2001US-0339453P.
2002US-0365091P.
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                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                           4.1%; Score 19;
100.0%; Pred. No.
tive 0; Mismatc
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The invention relates to isolated polynucleotide (I) and polypeptide (II) csequences. (I) is useful as hybridisation probes, polymerase chain (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cc genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is cuseful for generating antibodies against it, detecting or quantitating a cplypeptide in tissue, as molecular weight markers and as a food cc supplement. (II) and its binding partners are useful in medical imaging convolving aberrant protein expression or biological activity. The collypeptide and polynucleotide sequences have applications in collypeptide and polynucleotide sequences have applications in collypeptide and polynucleotide sequences have applications or responsible for genetic disorders or other traits to assess biodiversity cand to produce other types of data and products dependent on DNA and camino acid sequences ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at fig. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-639362/73.
N-PSDB; AAS70229.
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23-AUG-2000; 2000US-00649167.
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Query Match
Best Local S
Matches 19
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                                   Similarity
KORYRDILPYDSTRVPLGK 247
             4.1%;
_arity 100.0%;
Conservative
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                           Score 19; DB; Pred. No. 3.7
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3.7e-10;
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                                         Length 561
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Search completed: June Job time: 60 secs 18, 2004, 19:47:15

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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2
2: /cgn2_6/ptodata/2
3: /cgn2_6/ptodata/2
4: /cgn2_6/ptodata/2
5: /cgn2_6/ptodata/2
6: /cgn2_6/ptodata/2
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1 MSSPRKVRGKTGRD
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/cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
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/cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/BCTUS_COMB.pep:*
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US-08-449-609-9
US-08-685-992-26
US-09-361-096A-17
US-08-685-992-26
US-09-361-096A-11
US-08-449-609-11
US-08-449-609-15
US-08-036-210-15
US-08-036-210-15
US-08-036-210-22
US-08-449-609-22
US-08-449-609-22
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US-08-361-096A-25
US-08-361-096A-25
US-08-361-096A-25
US-08-361-096B-5
US-08-318-657-5
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sequence 9, Appli
sequence 26, Appl
sequence 27, Appl
sequence 11, Appl
sequence 11, Appl
sequence 11, Appl
sequence 15, Appl
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sequence 22, Appl
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Sequence 36, Appl
Sequence 9, Appli
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Sequence 9, Appli
Sequence 26, Appl
                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                             ; MOLECULE TYPE:
US-08-446-345-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Moller, Niels P.H.

APPLICANT: Moller, Niels P.H.

ITTLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE

TITLE OF INVENTION: PHOSPHATASES PTP-D1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Penn'-

STREFT.
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US-08-446-345-34
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Patent No.
       Query Match

Best Local Similarity 100.0%; Pred. No.
Matches 15; Conservative 0; Mismatc
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve;
CURRENT APPLICATION NUMBER: US/08/446,345
FILLING DATE: 22-MAY-1995
CLASSIFICATION DATA:
APPLICATION MUMBER: US 08/234,440
FILLING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COTUZI, LEUNABER: 30742
REFERENCE/DOCKET NUMBER: 7683-054
                                                                                                                                              TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                       TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: unknown
                                                                                                                                                                                        TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 10036-2711
                                                                                                                                  LENGTH:
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US-09-144-925-5
US-09-447-533-2
PCT-US95-05512-2
US-08-015-986A-2
US-08-015-986A-2
US-08-015-986A-2
US-08-342-930-4
US-08-342-930-4
US-08-342-930-4
US-08-015-985-5
US-09-280-597-6
US-09-280-597-7
US-09-280-597-7
US-09-280-597-7
US-09-280-597-7
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         Mismatches
   DB 2; ____
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Score

Word

Size

Searched:

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Title: Perfect score:

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                                                                                                                                                          US-08-036-210-9
GENERAL INFORMATION:
APPLICANT: Moller, NA
APPLICANT: Moller, Ka
APPLICANT: Ullrich, A
TITLE OF INVENTION: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                   Patent No. 55852
                                                                                                                                                                                                                                                                                                               Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGÝ: unknown
MOLECULE TYPE: protein
-08-446-345-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,345
FILING DATE: 22-MAY-1995
CITATION TOTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 30742
REFERENCE/COCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: {212}790-9990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/234,440
APPLICATION NUMBER: US 08/234,440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ullrich, Axel
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASES PTP-D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York STATE: N.Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                           391 PLLVHCSAGVGRTGV 405
                                                                                                                                                                                                                                                                                                             ch 3.2%; Score 15; DB 2; Similarity 100.0%; Pred. No. 5.8e-0 15; Conservative 0; Mismatches
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                                                                                                                                      Application US/08036210
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1174 amino acids
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                                                           Moller, Niels P.H.
Moller, Karin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
    PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE
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Best Local Similarity 100.0%; F
Matches 14; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 23-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683
TBLECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                              STREET: 1155 Avenue of CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Moller, N
APPLICANT: Moller, E
APPLICANT: Ullrich,
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICATION NUMBER: US/08/449,609
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/036,210
FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,210
FILING DATE: 23-MAR-1993
                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
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STREET: 1155 Avenue of the Americas
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STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 212-190-1911
TELEPHONE: 212-869-8864/9741
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Moller, Karin B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.0%; Score 14;
100.0%; Pred. No.
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hes 0;
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RESULT 6
US-08-685-992-26
; Sequence 26, Application US/08685992
; Patent No. 5912138
; Patent No. 5912138
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US-09-361-096A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.0%; Sometimes 100.0%; In Matches 14; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 08/449,609
PRIOR FILING DATE: 1995-05-24
PRIOR APPLICATION NUMBER: 08/036,210
PRIOR FILING DATE: 1995-03-23
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ULLRICH, AXEL
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE
FILE REFERENCE: 038602/0686
CURRENT APPLICATION NUMBER: US/09/361,096A
CURRENT FILING DATE: 1999-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: amino acid sequence OTHER INFORMATION: encoded by PCR fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 176
TYPE: PRT
                    TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN TITLE OF INVENTION: TYROSINE PHOSPHATASES NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS:
                                                                                             APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPAX: 212-869-8864/9741
  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAME: Misrock, S. I. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                          394 VHCSAGVGRTGVFI 407
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                                                                                                                                                                                                                                                                     79 VHCSAGVGRTGVFI 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLLER, KARIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLLER, NIELS P.H.
                                                                                                                                                                                                                                                                                                                                              Conservative
HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S. Leslie
                                                                                                                                                                                                                                                                                                                                                              3.0%; Score 14; DB 4; Length 176; 100.0%; Pred. No. 9.3e-06;
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                                                                                                                                                                                                                                                                                                                                            Patent No. 572...
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TONKS, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
TITLE OF SROUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/09144925 Patent No. 5951979
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                                                                                                    COUNTRY: USA
ZIP: 02421-4799
ZIP: 02421-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FactSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 245 amino acid
               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0)
FILING DATE: July 25,
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS,
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEPAX: 781-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,992
FILING DATE: 25-JUL-1996
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                 STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 245 amino acids
TYPE: amino acid
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linear
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100.0%; Pred. No. 1.3e-05;
               08/685,992
5, 1996
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; OTHER INFORMATION: Description of Artificial Sequence: PTP-S31D US-09-361-096A-47
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US-09-361-096A-47
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                                                                                                                                                                                US-08-036-210-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 47
LENGTH: 289
                                                                                                                                                  Sequence 11,
Patent No. 5
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                               Query Match
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1995-05-24
PRIOR APPLICATION NUMBER: 08/0
PRIOR FILING DATE: 1995-03-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 038602/0686
CURRENT APPLICATION NUMBER: US/09/361,096A
CURRENT FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 08/449,609
PRIOR FILING DATE: 1995-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MOLLER, KARIN B.
APPLICANT: ULLRICH, AXEL
APPLICANT: ULLRICH, AXEL
AND OF INVENTION: PTS-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                             APPLICANT:
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                                               TITLE OF INVENTION:
                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100
nes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 245 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 781-861-62.
TELEPAX: 781-861-9540
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                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 VHCSAGVGRIGVFI 407
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                                 OF SEQUENCES:
                                                                                                                                                1, Application US/08036210 5585233
                                                                                                                                                                                                                                               VHCSAGVGRTGVFI 234
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                                 Ulirich, axel
AVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
AVENTION: PHOSPHATASE
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                               Moller, Niels P.H. Moller, Karin B.
PENNIE & EDMONDS
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100.0%; Pred. No.
ative 0; Mismatci
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100.0%; Pred. No. 1.5e-(
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3R: CSHL96-03Z
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US-08-449-609-11
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Best Local Similarity 100.0%; P
Matches 14; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
            APPLICATION NUMBER: US/08/449,609
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/036,210
FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAMB: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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LENGTH: 322 amino acid
                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 322 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 23-MAI CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                              STREET: 1155 Ave
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212-190-19741
TELEPHONE: 212-869-8864/9741
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ZIP: 10036-2711
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                      B: PENNIE & EDMONDS
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moller,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moller, Niels P.H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Karin
                                                                                                                                                                                                                                                                                                                                                                                                                          PTP-831: A NOVEL PROTEIN TYROSINE PHOSPHATASE
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Pred. No.
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APPLICANT: WOLLER, KARIN B.
APPLICANT: WOLLER, KARIN B.
APPLICANT: WLLRICH, AXBL
ITITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE
FILE REFERENCE: 03660Z/0686
CURRENT APPLICATION NUMBER: US/09/361,096A
CURRENT APPLICATION NUMBER: US/09/361,096A
CURRENT FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 08/449,609
PRIOR APPLICATION NUMBER: 08/449,609
PRIOR APPLICATION NUMBER: 08/036,210
PRIOR APPLICATION NUMBER: 08/036,210
PRIOR APPLICATION NUMBER: 08/036,210
SOFTWARE: PASCHILL 1995-03-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PASCHILL VET: 2.1
                                                                                                                                                                                                                                                              RESULT 12
US-09-361-096A-15
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US-09-361-096A-11
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                        Sequence 15, Application US/09361096A Patent No. 6492495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Applicat Patent No. 6492495
GENERAL INFORMATION:
SENERAL INFORMATION:
SENERAL INFORMATION:
APPLICANT: MOLLER, KARIN B.
APPLICANT: MOLLER, KARIN B.
APPLICANT: MOLLER, KARIN B.
APPLICANT: MOLLER, KARIN B.
APPLICANT: ULLRICH, AXEL
TITLE OF INVENTION: PTP-531: A NOVEL PROTEIN TYROSINE PHOSPHATASE
FILE REFERENCE: 038602/0686
CURRENT APPLICATION NUMBER: US/09/361,096A
CURRENT FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-05-24
PRIOR FILING DATE: 1995-05-24
PRIOR FILING DATE: 1995-05-24
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Best Local Similarity
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 322 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 212-/50-000 TELEPHONE: 212-869-8864/9741
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100.0%; Pr
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US-08-036-210-15
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-361-096A-15
                                                                                                                  US-08-036-210-15
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; NUMBER OF SEQ ID NOS
; SOFTWARE: Patentin
; SEQ ID NO 15
                                               Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/036,210
PILING DATE: 23-MAR-1993
CLASSIFEICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION UMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-025
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Best Local Similarity
Matches 14; Conserval
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE TITLE OF INVENTION: PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Moller, Niels
APPLICANT: Moller, Karin
APPLICANT: Ullrich, Axel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
                                                                                                                                           LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                      TELEFAX:
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                           394 VHCSAGVGRTGVFI 407
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1155 Avenue of the Americas
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                                                         Conservative
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)S: 53
                              3.0%; 5c.
100.0%; Pr
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%; Pred. No. 2e-
0; Mismatches
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, 2e-05;
                                                                     DB 1;
2e-05;
                                                                                    Length 402;
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RESULT 14 US-08-449-609-15

Sequence 15, Application US/08449609

Patent No.

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RESULT 15
US-08-036-210-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEY 66141 PENNIE
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                          Patent No. 5585233
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Moller, Karin B.
APPLICANT: Ullrich, Axel
APPLICANT: Ullrich, Axel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/449,609
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/036,210
FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Moller, Niels P.H. APPLICANT: Moller, Karin B. APPLICANT: Ullrich, Axel
                                                                                                                                                                                                                TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE TITLE OF INVENTION: PHOSPHATASE NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                      COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                     CITY: New York
                                                                                                                                                       STREET:
                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 VHCSAGVGRTGVFI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 VECSAGVGRTGVFI 407
                                                                                                            New York
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1155 Avenue of the Americas
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VENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
VENTION: PHOSPHATASE
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 898 amin
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT ARPLICATION DATA:
APPLICATION NUMBER: US/08/036,210
FILING DATE: 23-KAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT_INFORMATION:
                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                 / Match 3.0%; Score 14; DB 1; I
Local Similarity 100.0%; Pred. No. 4.3e-05;
1es 14; Conservative 0; Mismatches 0;
                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                               NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-025
                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                           394 VHCSAGVGRTGVFI 407
797 VHCSAGVGRIGVFI 810
                                                                                                                                                                                unknown
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                                                                                                                                                                                              single
                                                                     0; Indels
                                                                                                        Length 898;
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Search completed: June 18, 2004, 19:49:51 Job time : 23 secs

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Minimum
Maximum
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
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Bd
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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(without alignments)
2723.150 Million cell updates/sec
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/ cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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## ALIGNMENTS

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Publication No. US20030095970A1

GENERAL INFORMATION:
APPLICAMT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPTPOS AND
TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 25
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNBER:
FILING DATE:
FILING DATE:
ATTORNSY/AGENT INFORMATION:
ANAMS: WALTHUTS, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCS/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                          ZII: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                       OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth
STREET: Suite 4700
                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A. ZIP: 90071-2066
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STATE: California
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APPLICANT: Plowman,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09095478 Publication No. US20030095970A1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                      NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                  ADDRESSEE: Lyon & Lyon
STREET: 633 West Pifth S
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
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VENTION: NOVEL PROTEIN TYROSINE
VENTION: PHOSPHATASE SuPTPO5 AND
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METHODS
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Sequence 8, Application US/09095478

Publication No. US2003095970A1

GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
ITILE OF INVENTION: HOUSEL PROTEIN
ITILE OF INVENTION: RELATED PRODUCTION OF INVENTION: RELATED PRODUCTION OF INVENTION: METHODS
INVESTED FROM DRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700

NOVEL PROTEIN TYROSINE PHOSPHATASE SUPTPOS AND RELATED PRODUCTS AND METHODS

AND

STREET: STREET: CITY: Lo

RESULT 3 US-09-095-478-8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard J.
REGISTRATION NUMBER: 23,327
REFERENCE/POCKET NUMBER: 224/
TELECOMMUNICATION INFORMATION:
TELEPRONE: (213) 489-1600
TELEPAR: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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NAME: Warburg, Richard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
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TKEQYQFCYSIVLEVLQNLLALY 463
                                                                                    RYVRKSHITGPLLVHCSAGVGRTGVPICVDVVPSAIBKNVSFDIMNIVTQMRKQRCGMIQ 440
                                                                                                                                                                                                             NHEEEYPYIATQGPLPETIEDFWQWYLENNCNVIAMITREIECGVIKCYSYWPISLKEPL
                                                                                                                                                                                                                                                                          DIIREFLELEQMTLPDDFNSGNTLQNRDKNRYRDILFYDSTRVPLGKNKDYINASYIRIV
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                                                                EFEHFSVELETFHVTQYETVRVEQIVKKSTGKSQCVKHLQETKWPDHGTPASADFFIKYV
                                                                                                                                                EFEHFSVETLETFHYTQYFTVRVEQIVKKSTGKSQCVKHLQFTKWDDHGTDASADFFIKYV
                                                                                                                                                                                           NHEEBYFYIATQGPLPETIEDFWQMVLENNCNVIAMITREIBCGVIKCYSYWPISLKEPL
                                                                                                                                                                                                                                                         DIIREFLELEQMTLPDDENSGNTLQNRDKNRYRDILPYDSTRVFLGKNKDYINASYIRIV
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                                                                           RESULT 4
US-09-095-478-3
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Sequence 3, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Simi
Matches 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Dish
MEDIUM TYPE: storage
MEDIUM TYPE: IBM Compatik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: IBM P.C. DOS
SOFTWARE: FASTSEQ for WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,
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LENGTH: 379 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKT NUMBER: 224
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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COUNTRY:
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                                                                                                                                         EQYOFCYETVLEVLONLLA 379
                                                                                                                                                           EQYOFCYBIVLEVLONLLA 461
                                                                                                                                                                                                   VRKSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 360
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linear
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100.0%; Pred. No. 0;
tive 0; Mismatches
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   Gregory
NOVEL PROTEIN TYROSINE
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US-09-095-478-3
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SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid single
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Best Local :
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ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOPTWARE: FASTENCY OF WINDOWS 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
FILING DATB:
CLASSIFICATION:
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MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
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TITLE OF INVENTION:
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STREET: Suite 4700
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California
                              TK 442
                                                                                    RYVRKSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQ
                                                                                                                                          BPEHFSVFLETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYV
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      X
                                                                RYVRKSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQ 403
                                                                                                                            EFEHFSVFLETFHVTQYFTVRVFQIVKKSTGKSQCVXHLQFTKWPDHGTFASADFFIKYV
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      405
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linear
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RELATED PRODUCTS ANI
METHODS
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                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Pred. No.
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Gaps

343 380 283

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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09095478 Publication No. US20030095970A1
                                                                                                                                                                                                                                                                                                                                          Matches
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 354 amino acids
TYPE: amino acid
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STATE: California
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                   348
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KSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGVFI 407
                                                   ENNCNVIAMITREIECGVIKCYSYWPISIKEPLEFEHFSVFLETFHVTQYFTVRVFQIVK 240
                                                                          ENNCNVIAMITREIECGVIKCYSYMPISLKEPLEFEHPSVFLETFHVTQYFTVRVFQIVK 347
                                                                                                                            DKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQMVL 180
                                                                                                                                                                                               LTQLAQIRELIFNSSARSAMRDCLNTLQKKEELDIIREFLBLEQMTLPDDFNSGNTLQNR
                                                                                                                                                                                                                                                                     PEPLESDIDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDTETSVSEKE
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                                                                                                                                                                                                                                                                                                                                        76.5%; Score 354; DE ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
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linear
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US-09-095-478-4
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US-09-095-478-4
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Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman
                                                                                                                                                                                           Matches
                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WAIPBURG, RICHARD J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: PASKEEQ for Windows 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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STREET: 633 West Fifth S
STREET: Suite 4700
CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                    TYPE: amino a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 90071-2066
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                              401
                                                                                         341 RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGV
                                                                                                                                           281 DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTV
121 GR 122
                                                                                                                                                                                           122;
                                                               61
                                                                                                                          1 DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVPLETFHVTQYFTV
                                                                                                                                                                                                           Similarity
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                              GR 402
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                                                             RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGV
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WENTION: NOVEL PROTEIN TYROSINE
WENTION: PHOSPHATASE SUPPPOS AND
NVENTION: RELATED PRODUCTS AND
NVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                        122 amino acids
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                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                         Peptide
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                                                                                                                                                                                                       26.3%; Score 122; DB 10; 100.0%; Pred. No. 1.6e-112;
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RESULT 7
US-09-095-478-22
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US-09-095-478-23
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Publication No.
                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (213) 955-04.
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
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MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 22.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
              CORRESPONDENCE ADDRESS
ADDRESSEE: Lyon & Ly
STREET: 633 West Fil
                                                                                APPLICANT: Plowman, Gregory
TITLE OF INVENTION: MOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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APPLICATION NUMBER:
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                                                                     NUMBER OF SEQUENCES:
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STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
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TOPOLOGY: lir
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TELEFAX: (213) 955-0440
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ZIP: 90071-2066
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                                                                                                                                                                                                                                                                                                             213 TLPDDFNSGNTLQNRDKNRYRDILPYDSTR 242
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E: Lyon & Lyon
633 West Fifth Street
Suite 4700
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PRIVION: NOVEL PROTIEN TYROSINE
PHOSPHATASE SUPTPOS AND
FENTION: RELATED PRODUCTS AND
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-09-095-478-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: PastSEQ for Windows 2.0 CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
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APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
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OPERATING SYSTEM:
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STREET: 633 West Pifth Street
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: California
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California
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VENTION: NOVEL PROTEIN TYROSINE
VENTION: PHOSPHATASE SUPTPOS AND
VENTION: RELATED PRODUCTS AND
VENTION: METHODS
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Gaps

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RESULT 10
US-09-095-478-25
TELEPHONE: (213) 905-0440
TELEPHONE: (213) 955-0440
TELEX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 29 milno acids
TYPE: amino acids
TYPE: amino acids
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SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Plowman,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity
Matches 29; Conserv
                                                                                                                 PILING DATE:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
NAME: Warburg, Richard J.
REGISTRATION UNMBER: 32,327
REGISTRATION UNMBER: 224/1
TELECOMMUNICATION INFORMATION:
TTLECOMMUNICATION 10FORMATION:
TTTLECOMMUNICATION 10FORMATION:
TTTLECOMMUNICATION 10FORMATION:
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Publication No.
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 22:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 633 West FI.
STREET: Suite 4700
CITY: Los Angeles
STATE: California
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APPLICATION NUMBER:
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TELEFAX: (213) 955-0440
TELEX: 67-3510
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FILING DATE:
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633 West Fifth Street
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7.4e-21;
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                                                                                                                    ; MOLECULE TYPE: Peptide US-09-095-478-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-095-478-5
                                                 Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                              TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bequence 5, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
Apprication
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
ATME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Plowman, Gregory
TITLE OF INVENTION: PHOSPHA
TITLE OF INVENTION: PHOSPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                             LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 WDVSDRSLRNRWNSMDSBTAGPSKTVSPV 148
                           374 DEFIKYVRYVRKSHITGPLLVHC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
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DFFIKYVRYVRKSHITGPLLVHC 116
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                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RELATED PRODUCTS AND METHODS
25
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                                                                                                                                                                                                                                                                                                                                                                                                                                         US/09/095,478
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                                                           0; Mismatches
                                                                      Score 23;
Pred. No.
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                                                                        DB 10; 1
2.4e-14;
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RESULT 12 US-10-311-764-4

Sequence 4, Application US/10311764 Publication No. US20040023245A1

INC.; AU-YOUNG, Janice K.

Ameena R.

April J.A.

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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040023245A1 7476861CD1
US-10-311-764-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/213,746
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 60/215,210
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/216,529
PRIOR FILING DATE: 2000-07-06
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
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Best Local S
                                                                 SEQ ID NO 1082
LENGTH: 1105
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SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                          Sequence 1082, Application US/10296115
Publication No. US20040053248A1
GENERAL INFORMATION:
                                                                                                         APPLICANT: Hyseq Inc
TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 7084PCT
CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
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PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, APPLICANT: BAUGHN, Mariah R.; DING, Ii APPLICANT: ELLIOTT, Vicki S.; GANDHI, Ameen APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, A APPLICANT: KEARNEY, Liam; LEE, Ernestine A. APPLICANT: LT VAN NOTION FORMATION APPLICANT LT VAN NOTION FORMATION APPLICANT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US01/19442
PRIOR PILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/212,447
PRIOR FILING DATE: 2000-06-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 420
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: PI-0126 USN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: CHAWLA, Narinder K.; YANG, Junming PPLICANT: YAO, Monique G.; YUE, Henry TILE OF INVENTION: PROTEIN PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT:
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                      TYPE: PRT
ORGANISM: Homo sapiens
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 KWRYRDILPYDSTRVPLGK 204
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THORNTON, Michael B.; TRIBOULBY, Catherine M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LU, Yan; NGUYEN, Danniel B.
ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
REDDY, Roopa M.; SANJANWALA, Madhusu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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k; Pred. No. 6.8
0; Mismatches
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SANJANWALA, Mac
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/10314232
Publication No. US20030138932A1
GENERAL INFORMATION:
APPLICANT: MOLLER, NIELS P.H.
APPLICANT: WOLLER, KARIN B.
APPLICANT: ULLRICH, AXEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 207
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 191, Applic
Publication No. US20
GENERAL INFORMATION:
                                                                                                              SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: MINASES IDENTIFIED WITH THE METHOD
FILE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
FILE REFERENCE: 038602/1543
CURRENT APPLICATION NUMBER: US/10/334,143
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: 60/343,169
PRIOR FILING DATE: 2001-12-31
PRIOR FILING DATE: 2001-12-31
                                                                                                                                                                                                                    APPLICANT: ULLRICH, AXEL
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE
FILE REFERENCE: 038602/0686
CURRENT APPLICATION NUMBER: US/10/314,232
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US/09/361,096
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1995-05-24
PRIOR FILING DATE: 1995-05-24
PRIOR FILING DATE: 1995-05-24
                                                                                                                                                                                PRIOR APPLICATION NUMBER: 08/036,210 PRIOR FILING DATE: 1995-03-23
                                                                                                                                                          NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH APPLICANT: SUDARSANAM, SUCHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 162
TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: (1)...(1105)
OTHER INFORMATION: Xaa = any amino acid or other as shown in Table 3
                   ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: amino acid sequence
                                                                    TYPE: PRT
                                                                                        ENGTH: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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; Pred. No.
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; OTHER INFORMATION: encoded by PCR fragment
US-10-314-232-9

Query Match.

Best Local Similarity 100.0%; Score 14; DB 14; Length 176;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 394 VHCSAGVGRTGVFI 407

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Db 79 VHCSAGVGRTGVFI 92

Search completed: June 18, 2004, 19:54:43

Job time: 49 secs
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Result
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Maximum DB seq
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    protein search, using sw model

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ALIGNMENTS

C;Accession: 138140

R;Moller, N.P.; Moller, K.B.; Lammers, R.; Kharitonenkov, A.; Sures, I.; Ullrich, R;Moller, N.P.; Moller, K.B.; J. 1994

A;Title: Src kinase associates with a member of a distinct subfamily of protein-ty A;Reference number: 138140; MUID:9432933; PMID:7519780

A;Reference number: 138140; MUID:9432933; PMID:7519780

A;Residence: 138140; MUID:9432933; PMID:7519780

A;Residence: 1.1914 (RES)
A;Residues: 1.1174 (RES)
A;Cross-references: EMBL:X79510; NID:9532055; PIDN:CAA56042.1; PID:9532056
A;Cross-references: EMBL:X79510; NID:9532055; PIDN:CAA56042.1; PTD:9532056
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-binding domain homology cp841>
F;25-304/Domain: protein 4.1 membrane-binding domain homology cp841>
F;31108/Active site: Cys (phosphorysteine intermediate) #status predicted
F;1114/Binding site: substrate phosphate (Arg) #status predicted A,Reference number: Z16472
A,Accession: T08716
A,Molecule type: mRNA
A,Residues: 1-398 <ANS>
A,Cross-references: EMBL:AL050040
A,Experimental source: fetal kidney; clone DKFZp566K0524
C;Genetics: protein-tyrosine-phosphatase (EC 3.1.3.48) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 22-Jun-1999 C;Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 22-Jun-1999 C;Accession: I38140 S A;Note: DKFZp566K0524.1 C;Superfamily: protein-tyrosine-phosphatase homology F;161-379/Domain: protein-tyrosine-phosphatase homology <PTP> protein-tyrosine-phosphatase homolog
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence\_revisic 문 R;Ansorge, W.; Wirkner, Usubmitted to the Protein C; Accession: T08716 I38140 RESULT Query Match Best Local S Matches 19 Species: Homo sapiens (man)
;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 13-Aug-1999 Query Match Best Local Similarity N 164 KWRYRDILPYDSTRVPLGK 182 W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. to the Protein Sequence Database, May 1999 19; Similarity KNRYRDILPYDSTRVPLGK 247 Conservative 100.0%; --3.2%; 100.0%; Score 19; ; Pred. No. Score 15; Pred. No. Mismatches DKFZp566K0524.1 - human (fragment) DB 2; 4e-11; DB 2; L: 0 Length 398; Length 1174; Indels A.; Sures, I.; Ullrich, 0 of protein-tyrosin Gaps 0 membranephosphata:

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protein tyrosine phosphatase -
C;Species: Mus musculus (house
C;Date: 26-Jul-1996 #sequence_1
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C;Superfamily: prote
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R;Title: Identification of a novel protein tyrosine phosphatase with sequence A;Reference number: S51005; MUID:95104449; ZMID:7805871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein-tyrosine-phosphatase (EC 3.1.3.48) 2E -
C,Species: Rattus norvegicus (Norway rat)
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A; Residues: 1-1176 < RES>
A; Cross-references: GB:D
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A; Residues: 840-1175
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A;Residues: 1-1175 <LAA>
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Date: 26-Jul-1996 #sequence_revision
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;1116/Binding
                                            ;923-1158/Domain:
                                                                                Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein; 
Keywords: phosphoprotein
                                                                                                                                                                                                                                                                          Reference number: I58345; MUID:95140431; PMID:7838537;
                                                                                                                                                                                                                                                                                                                                                                              Accession: I58345
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                                      25-304/Domain: protein 4.1 membrane-binding domain homology <B41>923-1158/Domain: protein-tyrosine-phosphatase homology <PTP2>
                        1110/Active site:
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larity 100.0%; Pred. No.
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  substrate phosphate
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Query Match

3.28;

Score 15;

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Length 1176;

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protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type f - mouse (fragment) N;Alternate names: leukocyte antigen-related protein LAR (;Species: Mus musculus (house mouse) C;Date: 03-Oct-1995 #sequence_revision 09-Mar-1996 #text_change 23-Jul-1999 C;Accession: A57068; $40280 R;Schaapveld, R.Q.J.; van den Maagdenberg, A.M.J.M.; Schepens, J.T.G.; Olde Weghuis, D. Genomics 27, 124-130, 1995 A;Fitle: The mouse gene Ptprf encoding the leukocyte common antigen-related molecule LA; Reference number: A57068; MUID:95394448; PMID:7665159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane F;1-582/Domain: leukocyte common antigen cytosolic domain homology (fragment) <LAC> F;50-271/Domain: protein-tyrosine-phosphatase homology <PTP1> F;339-562/Domain: protein-tyrosine-phosphatase homology <PTP1> F;339-562/Domain: protein-tyrosine-phosphatase homology <PTP2>
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C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
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A; Residues: 116-221 <HEN>
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submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:Z37988; NID:g993005; PIDN:CAA86070.1; PID:g993006 R;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
                                                                                                                                                                                                submitted to the EMBL Data Library, March 1995 concerns to the EMBL Data Library, March 1995 conceptor-like
                                                                                                                                                                                                                                                                                              N;Alternate names: leukocyte antigen-re
C;Species: Anopheles gambiae (African n
C;Date: 08-Jul-1995 #sequence_revision
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A; Introns: 1026/3; 1070/3; 1209/3
C; Superfamily: leukocyte antigen-related protein;
                                                                     A;Molecule type: DNA
A;Residues: 1-1231 <SPI>
A;Cross-references: EMBL
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A; Accession: S53089
                                                  C;Genetics:
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14; Conserv
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                                                                          EMBL: X85217; NID: 9732549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.0%;
                                                                                                                                                                                                                                                                                                                           (EC 3.1.3.48) AnIAR - African malaria antigen-related protein (African malaria mosquito)
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thes 0;
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                                                                                PIDN: CAA59483.1;
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                                                                          PID:9732550
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     III repeat homology;
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leucocyte common antigen-related protein (LAR) - rat (fragment)
N;Alternate names: LAR receptor-linked tyrosine phosphatase
N;Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)
C.Species: Rattus norvegicus (Norway rat)
C;Date: 02-Unl-1996 #sequence_revision 02-Unl-1996 #text_change 21-Unn-2000
C;Accession: A56493; I55393
R;Znhang, U.S.; Longo, F.M.
J. Cell Biol. 128, 415-431, 1995
A;Title: LAR tyrosine phosphatase receptor: alternative splicing is preferen
A;Reference number: A56493; MUID:95146548; PMID:7844155
A;Accession: A56493; MUID:95146548; PMID:7844155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Longo, F.M.; Martignetti, J.A.; Le Beau, J.M.; Zhang, J.S.; Barnes, J.P.; Brot J. Biol. Chem. 268, 26503-26511, 1993
A;Title: Euckocyte common antigen-related receptor-linked tyrosine phosphatase. A;Reference number: 155393; MUID:94075340; PMID:8253779
A;Accession: 155393
C;Accession: A48758
R;Pan, M.G.; Rim, C.; Lu, K.P.; Florio, T.; Stork, P.J.S.
J. Biol. Chem. 268, 19284-19291, 1993
A;Title: Cloning and expression of two structurally distinct
A;Fitle: Cloning and expression of two structurally distinct
A:Reference number: A48758; MUID:93374907; PMID:8396131
                                                                                                                                       protein-tyrosine-phosphatase (EC 3.1.3.48), receptor-linked form P1 precursor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A48758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;X
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F;618-1231/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;988-1211/Domain: protein-tyrosine-phosphatase homology <PTP
F;987/Active site: Cys (phosphocysteine intermediate) #status predicted F;1163/Active site: Cys (phosphocysteine intermediate) #status predicted F;1163/Birding site: substrate phosphate (Arg) #status predicted
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F;667-1290/Domain: leukocyte common antigen cytosolic domain homology <1AC>
F;667-1290/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1047-1270/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;931/Active site: Cys (phosphocysteine intermediate) #status predicted F;937/Binding site: substrate phosphate (Arg) #status predicted F;1222/Active site: Cys (phosphocysteine intermediate) #status predicted F;1228/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 831-1290 <AE2>
A;Cross-references: EMBL:U00477; NID:g392565; PIDN:AAC04306.1; PID:g392566
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat
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Best Local
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larity 100.0%; Pred. No.
Conservative 0; Mismatc
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Pred. No.
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hes 0;
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RESULT I58148

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F;148-208/Domain: immunoglobulin homology <IMM1>
F;245-299/Domain: immunoglobulin homology <IMM2>
F;245-299/Domain: immunoglobulin homology <IMM2>
F;317-399/Domain: fibronectin type III repeat homology <3FR>
F;881-1499/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1257-1479/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1257-1479/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1147/Binding site: substrate phosphate (Arg) #status predicted
F;1147/Binding site: Cys (phosphocysteine intermediate) #status predicted
F;1432/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1438/Binding site: substrate phosphate (Arg) #status predicted
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A;Reference number: ISO212; )
A;Accession: ISO212
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C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C;Accession: ISO212
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F/411-504/Domain: fibronectin type III repeat homology <FN3B>
F/411-504/Domain: fibronectin type III repeat homology <FN3B>
F/509-599/Domain: fibronectin type III repeat homology <FN3B>
F/600-684/Domain: fibronectin type III repeat homology <FN3B>
F/600-684/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F/1256-147/Domain: protein-typesine-phosphatase homology <FTP2>
F/1256-147/Domain: protein-typesine-phosphatase homology <FTP2>
F/140/Active site: Cys (phosphocysteine intermediate) #status predicted
F/1469/Active site: Sys (phosphocysteine intermediate) #status predicted
F/1429/Active site: Cys (phosphocysteine intermediate) #status predicted
F/1435/Binding site: substrate phosphate (Arg) #status predicted
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A; Residues: 1-1496 < PAN>
A; Cross-references: GB:L19180
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A;Status: preliminary
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Mech. Dev. 46, 201-217, 1994
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                                                                                                                                   Query Match
Best Local :
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                                                  394 VHCSAGVGRTGVFI 407
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                                                                                                                                   Similarity
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                                                                                                              Conservative
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immunoglobulin homology <IMM2>
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L00.0%; Pred. No.
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C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydre
R;47-109/Domain: immunoglobulin homology <IMMI>
R;447-109/Domain: immunoglobulin homology <IMMI>
R;449-209/Domain: immunoglobulin homology <IMMI>
R;246-300/Domain: immunoglobulin homology <IMMI>
R;4413-506/Domain: fibronactin type III repeat homology <3FR>
R;4413-506/Domain: fibronactin type III repeat homology <3FR>
R;482-1501/Domain: leukocyte common antigen cytosolic domain homology <LAC>
R;969-1190/Domain: protein-tyrosine-phosphatase homology <PTP1>
R;969-1190/Domain: protein-tyrosine-phosphatase homology <PTP2>
A; Molecule type: mRNA
A; Residues: 1-398, 799-1691 <MI2>
A; Experimental source: brain
A; Note: sequence inconsistant with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form D N;Altornate names: MPTP delta type D N;Contains: protein tyrosine phosphatase, receptor type delta, splice form A C;Species: Mus musculus (house mouse)
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F;1142/Active site: Cys (phosphocysteine intermediate) #link PTP1 #status predicted F;1148/Binding site: substrate phosphate (Arg) #link PTP1 #status predicted F;1433/Active site: Cys (phosphocysteine intermediate) #link PTP2 #status predicted F;1439/Binding site: substrate phosphate (Arg) #link PTP2 #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: D54689; A54689; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H. R;Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H. Mol. Cell. Biol. 13, 5513-5523, 1993
A;Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in s A;Reference number: A54689; MUID:93360986; PMID:8355697
A;Accession: D54689
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A;Residues: 1-1501 <ZHA>
A;Cross-references: EMBL:L12329; NID:g294573; PIDN:AAC37657.1; PID:g294574
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repo
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A;Note: in Genbank entry RATTYRPHOS, release 113.0, the source is design:
R;Zbang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
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A; Residues: 1-1501 <WAL>
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                                                                                                                                                                                                               Experimental source: brain;
Note: sequence inconsistent with nucleotide translation;
Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBIP:136537)
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Residues: 1-1691 <MIZ>
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C.Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hydrogy-cycle for the common antigen cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle for the cycle 
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A;Residues: 1-1788, 'G', 1790-1863 <GOL>
A;Residues: 1-1788, 'G', 1790-1863 <GOL>
A;Cross-references: EMBL:L11587; NID:g205134; PIDN:AAC37656.1; PID:g205135
R;Yan, H.; Grossman, A.; Wang, H.; D'Ebustachio, P.; Mossie, K.; Musacchio, J.M.
Biol. Chem. 268, 24880-24886, 1993
J. Biol. Chem. 268, 24880-24886, 1993
A;Title: A novel receptor tyrosine phosphatase-sigma that is highly expressed A;Reference number: A49104; MUID:94043351; PMID:8227050
A;Accession: A49104
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                                                                                                                   F;318-400/Domain: fibronectin type III repeat homology <FN3A>
F;413-499/Domain: fibronectin type III repeat homology <FN3B>
F;413-499/Domain: fibronectin type III repeat homology <FN3C>
F;1244-1863/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1331-1552/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1304/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1510/Jainding site: substrate phosphate (Arg) #status predicted
F;1795/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1795/Active site: Cys (phosphocysteine intermediate) #status predicted
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C;Superfamily: leukocyte antigen-valated rectains fit.
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F;27-1863/product: protein-tyrosine-phosphatase #status
F;149-209/Jomain: immunoglobulin homology <IMM1>
F;246-300/Domain: immunoglobulin homology <IMM2>
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A; Residues: 1-1863 < ZHA>
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; PMID:8068021
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C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hydrides from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the provided from the
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A; Residues: 1-352,'H',354-535,'S',537-601,1002-1894 <MI2>
A; Experimental source: brain; splice form C
A; Note: sequence inconsistent with nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBIP:136530)
                                                                                                                                                                                                                     R;Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H. J. Exp. Med. 168, 1523-1530, 1998
A;Title: A new member of the immunoglobulin superfamily that has a cy A;Reference number: JL0051; MUID:89035978; PMID:2972792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leukocyte antigen-related protein precursor - human N;Alternate names: leukocyte common antigen homolog N;Contains: protein-tyrosine-phosphatase (BC 3.1.3.48)
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A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:1374)
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A):Title: MPTP delta, a putative murine homolog of HPTP delta, is A;Reference number: A54689; MUID:93360986; PMID:8355697
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C;Date: 25-Apr-1995 #sequence_revision 19-May-1995 #text_change 12-Feb-1999
C;Accession: C54689; B54689
                                                     A; Molecule type: mRNA
A; Residues: 1-1897 < S'
                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
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A; Residues: 1-1894 < MIZ>
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                                                                                                                                 A; Status: nucleic acid sequence not
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N;Alternate names: leukocyte common antigen homolog N;Contains: protein-tyrosine-phosphatase (EC 3.1.3.48) C;Species: Rattus norvegicus (Norway rat) C;Date: 20-Feb-1995 #sequence_revision_20-Feb-1995 #teo;Accession: S46216; S23252; A41032; A33154 R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Gold Biochem. J. 302, 39-47, 1994
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F;403-489/Domain: fibronectin type III repeat homology <FN3A>
F;403-489/Domain: fibronectin type III repeat homology <FN3B>
F;508-685/Domain: fibronectin type III repeat homology <FN3D>
F;598-685/Domain: fibronectin type III repeat homology <FN3D>
F;698-798/Domain: fibronectin type III repeat homology <FN3F>
F;810-893/Domain: fibronectin type III repeat homology <FN3F>
F;905-989/Domain: fibronectin type III repeat homology <FN3G>
F;905-989/Domain: fibronectin type III repeat homology <FN3G>
F;101-1078/Domain: transmembrane #status predicted <IMT>
F;1275-1897/Domain: intracellular #status predicted <INT>
J. Biol. Chem. 266, 19688-19696, 1991
A;Title: Cloning, bacterial expression, purification, at A;Reference number: A41032; MUID:92011772; PMID:1918076
A;Accession: A41032
                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1361-1604;1649-1898 <HAS>
R;Pot, D.A.; Woodford, T.A.; Rembouts
                                                                                                                                                                                                                                                                                                                                                                                    R;Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.
Biochem. J. 284, 569-576, 1992
A;Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by threapers reference number: $23126; MUID:92287069; PMID:1599438
A;Accession: $23252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-1898 <ZHA>
A;Residues: 1-1898 <ZHA>
A;Cross-references: EMBL:Ll1586; NID:g205132; PIDN:AAC37655.1; PID:g205133
P·Hashimoto. N.; Zhang, W.R.; Goldstein, B.J.
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F;1275-1897/Domain: intracellular #status predicted <INT>
F;1275-1897/Domain: leukcoyte common legen cytosolic domain homology <IAC>
F;1285-1897/Domain: protein-tyrosime-phosphatase homology <PTP1>
F;1355-1586/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1554-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;144-97,146-197,243-288/Disulfide bonds: #status predicted
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C;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
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A;Cross-references: GDB:120138; OMIM:179590
A;Map position: 1p34-1p34
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F;236-290/Domain: immunoglobulin homology <IMM3>
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                                                                                                                                                                                       T.A.; Remboutsika, B.; Haun, R.S.; Dixon, J.E.
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C;Reywords: duplication; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; t;1-27/Domain: (or 1-26) signal sequence #status predicted <SIG>
F;1-27/Domain: (or 27-1898) leukocyte antigen-related protein #status predicted <MAT
F;28-1251/Domain: (or 27-1251) extracellular #status predicted <EXT>
F;48-1251/Domain: immunoglobulin homology <IMM1>
F;41-109/Domain: immunoglobulin homology <IMM2>
F;41-300/Domain: immunoglobulin homology <IMM3>
F;318-400/Domain: fibronectin type III repeat homology <FN3A>
F;318-499/Domain: fibronectin type III repeat homology <FN3B>
F;511-599/Domain: fibronectin type III repeat homology <FN3B>
F;610-695/Domain: fibronectin type III repeat homology <FN3B>
F;908-799/Domain: fibronectin type III repeat homology <FN3B>
F;108-799/Domain: fibronectin type III repeat homology <FN3B>
F;1052-1079/Domain: fibronectin type III repeat homology <FN3B>
F;1052-
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A;Accession: A33154
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Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 14; Conservative 0; Mismatches 0;
1828 VHCSAGVGRTGVFI 1841
                                                                                                                                                                        394 VHCSAGVGRTGVFI 407
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Search completed: June 18, 2004, 19:49:16 Job time: 22 secs

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Result
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Q62728 rattus norv
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P10586 homo sapien
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STRAIN-Sprague-Dawley;
MEDLINE-95104449; PubMed-7805871;
MEDLINE-95104449; PubMed-7805871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein tyrosine phosphatase, non-receptor type
(Protein-tyrosine phosphatase 2E).
PTPN21 OR PTP2E.
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DOMAIN
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01-NOV-1997
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                                              EMBL; U17971; AAA62153.1;
EMBL; U18293; AAA62154.1;
PIR; S51005; S51005.
HSSP; Q06124; 2SHP.
                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fantus G., Shen S.H.;
"Identification of a novel protein tyrosine phosphatase with sequence indentification of a novel proteins of the band 4.1 family.";
homology to the cytoskeletal proteins of the band 4.1 family.";
FEBS Lett. 356:351-356(1994).
-i- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
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                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                              Isord=Q62728-2; Sequence=VSP 000498;
TISSUE SPECIFICITY: ParticularTy abundantly in adrenal glands.
SIMILARITY: Contains 1 FERM domain.
SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tyrosine + phosphate.
ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                     European
                                                                                                                                                                                                                                                                                                                                             Non-receptor class subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through teen the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content
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PS600383; TYR PS6038BPTP; 1.
PS50055; TYR PHOSPHATASE 2; 1.
PS50056; TYR PHOSPHATASE 2; 1.
ps protein; Cytoskeleton; Hydrolase.
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  IPR000299; Band 4.1.
IPR000387; TYR phosphatase.
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POLY-GLU.
WW; 5772D9B1A99B3FDA CRC64;
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POLY-PRO.
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Pred. No. 4e-07;
Mismatches 0
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Pfam; PF00102; Y phosphatase; 1
PRINTS; PR00935; BAND41.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00295; B41; 1.
SMART; SM00194; PTPC; 1.
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01-NOV-1997
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PROSITE; PS00661; FERM 2; 1.

PROSITE; PS00057; FERM 3; 1.

PROSITE; PS00383; TYR PHOSCHATASE 1; 1.

PROSITE; PS00385; TYR PHOSCHATASE PTP; 1.

PROSITE; PS50056; TYR PHOSCHATASE 2; 1.

Structural protein; Cytoskeletma; Hydrolase; Alternative splicing.
                This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is no modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                           - I- FUNCTION: May be involved in the regulation of growth and differentiation of liver cells.
- I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = proteintyrosine + phosphate.
- I- TISSUE SPECIFICITY: Liver.
- I- SIMILARITY: Contains 1 FERM domain.
- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
- Non-receptor class subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein tyrosine phosphatase, non-receptor type
(Protein-tyrosine phosphatase PTP-RL10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE-95140431; PubMed=7838537;
Higashitsuji H., Arii S., Furutani M., Imamura M., Kaneko Y.,
Takenawa J., Nakayama H., Fujita J.;
Takenawa J., Nakayama H., Fujita J.;
"Enhanced expression of multiple protein tyrosine phosphatases in the
regenerating mouse liver: isolation of PTP-RL10, a novel cytoplasmic-
type phosphatase with sequence homology to cytoskeletal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Liver;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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15; Conservative
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(BY SIMILARITY).
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MGD; MGI:1334406; Ptpnzi.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000242; Tyr PP.
Ffam; PF00373; Band 41; I.
R Pfam; PF000102; Y phosphatase; 1.
R Pfam; PF000102; Y phosphatase; 1.
R Pfam; PF000102; Y phosphatase; 1.
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Best Local Similarity
Matches 15; Conserv
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PTPF_HUMAN STANDARI
P10586;
01-JUL-1989 (Rel. 11, 0
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domains
LAR.";
EMBO J.
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                                                                        MEDLINE=90316093; PubMed=1695146;
Streuli M., Krueger N.X., Thai T., Tan
"Distinct functional roles of the two
"Distinct functional roles of the two
                                                                                                                                                                                                                                                                                                    MEDLINE=90046860; PubMed=2554325;
Streuli M., Krueger N.X., Tsai A.Y.M.,
"A family of receptor-linked protein t
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE=89035978; PubMed=2972792;
Streuli M., Krueger N.X., Hall L.R., Schlossman S.F., Sai
"A new member of the immunoglobulin superfamily that has
cytoplasmic region homologous to the leukocyte common and
J. Exp. Med. 168:1523-1530(1988).
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PRINTS; PRO0700; PRTYPHPHTASE.
SMART; SM00295; B44; 1.
SMART; SM00194; PTPC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAR protein precursor PTPRF OR LAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Structural protein;
                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                         Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391 PLLVHCSAGVGRTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E; PS00660; FERM 1; 1.

B; PS00661; FERM 2; 1.

E; PS50057; FERM 3; 1.

B; PS00383; TYR PHOSPHATASE 1; 1.

B; PS0055; TYR PHOSPHATASE 7TP; 1.

B; PS50055; TYR PHOSPHATASE 2; 1.

ural protein; Cytoskeleton; Hydrolase.
                                                              of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLLVHCSAGVGRTGV 1119
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565
1176
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923
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                                                           receptor-linked protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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572
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308
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28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN-TYROSINE PHOSPHATASE PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-PRO
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                                                                                                                                                                                                                                                  86:8698-8702 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigen related)
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                                                 Tang M., Saito H.;
two intracellular phosphatase :
tein tyrosine phosphatases LCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1897
                                                                                                                                                                                                                                                                                                              tyrosine phosphatases
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                                                                                                                                                                                                                                                                                                                                        Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
4e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saito H.;
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SEQUENCE

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11844

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CRC64;

OF ACTIVITY

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Pfam; PP00041; fn3; 7.

Pfam; PP00047; ig; 3.

Pfam; PP00047; ig; 3.

Pfam; PP00102; Y_bhosphatase; 2.

Pfam; PR00104; FNTYPHPHTASE.

PRINTS; PR000104; FNTYPHPHTASE.

SMART; SM00106; FN3; 4.

SMART; SM00108; IGC2; 3.

SMART; SM00109; PTPC; 2.

SMART; SM00109; PTPC; 2.

SMART; SM00109; TYR; PHOSPHATASE 1; 2.

PROSITE; PS00383; TYR PHOSPHATASE 2; 2.

PROSITE; PS00056; TYR_PHOSPHATASE 7; 2.

PROSITE; PS00055; TYR_PHOSPHATASE 7; 2.

PROSITE; PS00055; TYR_PHOSPHATASE 7; 2.

PROSITE; PS00055; TYR_PHOSPHATASE 7; 2.

PROSITE; PS00055; TYR_PHOSPHATASE 7; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR008957; FN_III-like.
InterPro; IPR003961; FN_III.
InterPro; IPR003961; PNIIII subd.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; TYR_PP.
         CARBOHYD
CARBOHYD
CARBOHYD
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MUTAGEN
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TRANSMEM
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          883
                                                                                                   ACT_SITS
                                                                                                                                             DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005001; F:transmembrane receptor protein tyrosine
GO; GO:0007155; P:cell adhesion; TAS.
GO; GO:0007185; P:transmembrane receptor protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S03841; TDHULK.
PDB; 1LAR; 25-APR-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y00815; CAA68754.1; ~. PIR; S03841; TDHULK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>-</del>
                                                                                                                            ACT_SITE
                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                             Hydrolase; Rec
Cell adhesion;
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                                                                                                                                                                          DOMAIN
                                                                                                                                                                                     DOMAIN
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It possesses
(PTPAse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tyrosine + phosphate.

tyrosine + phosphate.

Type I membrane protein.

SUBCELIULAR LOCATION: Type I membrane protein.

SIMILARITY: Contains 3 immunoglobulin-like C2-type desimilarity: Contains 6 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 8 fibronectin type III domains.
SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: The first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the second one seems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC:9670; PTPRF.
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                                                                                                                               1251
1275
23
125
125
222
1360
1649
1538
                                                                                                       1829
           107
240
285
711
956
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                                                                                                                                             1897
1250
1274
1897
113
214
304
1606
1897
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                                                                                                                               1538
                                      107
240
285
711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           possible that DLAF
intrinsic protein
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         SIMILARITY).

N-LINKED (GI
N-LINKED (GI
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N-LINKED (GI
                                                                                                                                            IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
PROTEIN-TYROSINE PHOSPHATASE PROTEIN-TYROSINE PHOSPHATASE
                                                                                                       SIMILARITY).
PHOSPHOCYSTEINE
                                                                                                                                 PHOSPHOCYSTEINE INTERMEDIATE
                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                       LAR PROTEIN.
                                                                                                                                                                                                                                                                             tein; Signal; Transmembrane;
domain; Repeat; 3D-structur
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                        GLCNAC...
GLCNAC...
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(GLCNAC...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell adhesion receptor. ine phosphatase activity
                                                                                                       INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tic activity, where specificity of
                                       (POTENTIAL)
                                                     (POTENTIAL)
                                                                 (POTENTIAL)
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2:
(BY
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Matches 14
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                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase delta precursor
Genew; HGNC:9668; PTPRD. MIM; 601598; -. GO:0005887; C:integral
                                            EMBL; L38929; AAC41749.1; -.
EMBL; X54133; CAA38058.1; -.
PIR; A56178; A56178.
HSSP; P18052; 1YFO.
                                                                                                                                                                                                                                                                                                            -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine phosphatases
EMBO J. 9:3241-3252(1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krueger N.X., Streuli M., Saito H.;
"Structural diversity and evolution of human receptor-like protein
tyrosine phosphataees.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91006018; PubMed=2170109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.; "Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta. Evidence for tissue-specific expression alternative human transmembrane protein-tyrosine phosphatase delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND MUTAGENES
MEDLINE=95204468; PubMed=7896816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1991 (Rel. 20,
01-OCT-1996 (Rel. 34,
10-OCT-2003 (Rel. 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTPD_HUMAN
P23468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol.
                                                                                                                                                                                                                                           Isoid=P23468-2; Sequence=VSP_005147, VSP_005148, VSP_005149;
Name=3; Synonyms=Fetal brain;
Isoid=P23468-3; Sequence=VSP_005150;
Isoid=P23468-3; Sequence=VSP_005150;
PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN PROM THE TRANSMEMBRANE SEGENT:
SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 8 fibronectin type III domains.
SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     tyrosine + phosphate.
SUBCELLULAR LOCATION: Type I membrane protein
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=3; Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OJ. 9:3241-3252(1990).
CATALYTIC ACTIVITY: Protein tyrosine phosphate
                                                                                                                                                                                                                                                                                                                                                                                                          Name=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                          |sold=P23468-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF 390-1912 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VHCSAGVGRTGVFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VHCSAGVGRTGVFI 1840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chem. 270:6722-6728(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acentea
                                                                                                                                                                                                                                                                                                                                                                           Synonyms=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND MUTAGENESIS OF ARG-1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.0%;
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Catarrhini; Hominidae;
 plasma membrane;
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R Pfam; pF00047; ig; 3.

R Pfam; pF00102; Y phosphatase; 2.

R Pfam; pF00102; Y phosphatase; 2.

R PRINTS; pR000104; FNTYPHPHTASE.

R SMART; SM00060; FN3; 8.

R SMART; SM00104; PTCc; 2.

R SMART; SM00104; PTCc; 2.

R SMART; SM00104; PTCc; 2.

R PROSITE; PS50035; TYR PHOSPHATASE 1; 2.

R PROSITE; PS50055; TYR PHOSPHATASE 2; 2.

R PROSITE; PS50055; TYR PHOSPHATASE PTP; 2.

R PROSITE; PS50055; TYR PHOSPHATASE PTP; 2.

R PROSITE; PS50055; TYR PHOSPHATASE PTP; 2.

R PROSITE; PS50055; TYR PHOSPHATASE PTP; 2.

R PROSITE; PS50055; TYR PHOSPHATASE PTP; 2.

R PROSITE; PS50055; TYR PHOSPHATASE PTP; 2.
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Best Local &
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InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_PP.
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GO:0006470; 1
GO:0007185; 1
1842
                                 14;
                                          Similarity
           VHCSAGVGRTGVFI 407
VHCSAGVGRTGVFI 1855
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R->A: 2.5-FOLD REDUCTION IN
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IG-LIKE C2-TYPE
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RESULT 6
PTNS\_HUMAN

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"Protein-tyrosine phosphatase expression in pre Cancer Res. 52:737-740(1992).
-!- FUNCTION: Interacts with LAR-interacting pr -!- CATALYTIC ACTIVITY: Protein tyrosine phosph tyrosine + phosphate.
-!- SUBCELUTLAR LOCATION: Type I membrane prote -!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms-
Comment-Additional isoforms seem to exist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Fetal brain;

TISSUE-Fetal brain;

MEDLINB-96102179; PubMed-8524829;

Pulldo R., Serra-Pages C., Tang M., Streuli M.;

"The LAR,PTP delta/FTP sigma subfamily of transmembrane protein-
tyrosine-phosphatases: multiple human LAR, PTP delta, and PTP sig
isoforms are expressed in a tissue-specific manner and associate
the LAR-interacting protein LIP.1."

Proc. Natl. Acad. Sci. U.S.A. 92:11686-11690(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-126 FROM N.A.
Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Lamerdin J.E., McCready P.M., Dias J., Ramirez M., Stilwagen S.,
Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Phan H., Velasco N., Do L., Regala W., Terry A., Avila J., Liu
Banganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu
Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Arellano A., Carrano A.V.;
Sequence analysis of a 2.5 Mb region in 19p13.3.";
Submitted (CCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1503-1589 FROM N.A. MEDLINE=92119637; PubMed=1370651; Adachi M., Sekiya M., Arimura Y., Takekawa
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MEDLINE=96255038; PubMed=8992885;

Endo N., Rutledge S.J., Opas E.E., Vogel R., Rodan G.A., Schmidt A.

"Human protein tyrosine phosphatase-sigma: alternative splicing and inhibition by bisphosphonates.";

J. Bone Miner. Res. 11:535-543(1996).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Q13332; Q15
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sanotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Receptor-type protein-tyrosine phosphatase S p.
(R-PTP-S) {Protein-tyrosine phosphatase sigma}
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Name=PTPS-MBC;
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Name=PTPS-MEB;
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                                                                                                                                                                                                                                                                                                                          IsoId=Q13332-3; Sequence=VSP_050022,
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Q15718; Q16341;
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              Contains 3 immunoglobulin-like C2-type domain. Contains 8 fibronectin type III domains. Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                     Sequence=VSP_050024;
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i) (R-PTP-sigma).
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GO; GO:0005887; C:integral to plasma me GO; GO:0005001; F:transmembrane recepto InterPro; IPR008957; FN_III-like. InterPro; IPR003961; FN_III. subd. InterPro; IPR003962; FnIII subd. InterPro; IPR0031962; FnIII subd. InterPro; IPR0031963; Tyr_pp. IPR003598; Tyr_pp. IPR003598; Tyr_pp. IPR003647; Tyr_pp. IPR000387; Tyr_pp.
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EMBL; S78080; AAB21146.2; -.
HSSP; P18052; 1YFO.
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PROTEIN-TYROSINE PHOSPHAY
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Q15678;
                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Protein tyrosine phosphatase, non-receptor type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                      TISSUE=Breast carcinoma;
MEDLINE=95251727; PubMed=7733990;
Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A., Rogers M.V.,
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         PTPN14 OR PEZ.
                                                                                                                                                             tyrosine + phosphate.
                                                                                                                                                                                                                 "Pez: a novel human cDNA encoding protein tyrosine
                                                                                                                                                                                                        ezrin-like domains.";
                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                  Protein-tyrosine phosphatase pez).
                                                                                                                                                                                Chem. Biophys. Res. Commun. 209:959-965(1995).
CATALYTIC ACTIVITY: Protein tyrosine phosphat
                                                                                                                 including kidney, skeletal muscle, lung and SIMILARITY: Contains 1 FERM domain. SIMILARITY: Belongs to the protein-tyrosine Non-receptor class subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394
                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
 X82676; CAA57993.1;
JC4155; JC4155.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VHCSAGVGRTGVFI 1891
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1196
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100.0%;
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                                                                                                                                                               Expressed in a variety of human tissues
                                                                                                                                                                                   Protein tyrosine phosphate +
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F -> 9
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7 -> HP (IN REF. 2).
SA -> RP (IN REF. 2).
LGPV -> RSPA (IN REF. 2).
GAEGRGPPR. -> RREARGRRS (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VSP_050024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAEPGAENAV -> GRLSRARRTL (IN REF. 2).
TV -> SL (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Missing (in isoform PTPS-MEB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTId=VSP
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D (IN REF. 4).
A (IN REF. 4).
K (IN REF. 2).
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7.3e-06;
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                                                                                                                               phosphatase family.
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RESULT 8
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Best Local
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InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000242; Tyr pp.
Pfam; PF000773; Band 41; I.
Pfam; PF00102; Y phosphatase; 1.
PRINTS; PR00935; BAND41.
PRINTS; PR009305; BRITYPHPHTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
SEQUENCE
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ACT_SITE
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PROSITE; PS00661; PERM_2; 1.

PROSITE; PS50057; PERM_3; 1.

PROSITE; PS00383; TYR_PHOSPHATASE_FIP; 1.

PROSITE; PS50055; TYR_PHOSPHATASE_FIP; 1.

PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.

Structural protein; Cytoskeleton; Hydrolase.
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SMART; SM00194; PTPc; 1.
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GO; GO:0006470;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP;
                                                                                                                                        MEDIINE=94354845; PubMed=8074693; Sawada M., Ogata M., Fujino Y., Hamaoka T.; Sawada M., Ogata M., Fujino Y., Hamaoka T.; Sawada M., Ogata M., Fujino Y., Hamaoka T.; Contoning of a novel protein tyrosine phosphatase with homology to cytoskeletal protein 4.1 and its expression in T-lineage cells."; biochem. Biophys. Res. Commun. 203:479-484(1994).

Biochem. Biophys. Res. Commun. 203:479-484(1994).

-I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
[Protein-tyrosine phosphatase PTP36].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew;
                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                tyrosine + phosphate.
-!- TISSUE SPECIFICITY: Thymus;
                                                                                                                                                                                                                                     STRAIN=CB-17-SCID;
                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
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DOMAIN
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                           non-hematopoletic origins.
SIMILARITY: Contains 1 FERM domain.
SIMILARITY: Belongs to the protein-tyrosine
Non-receptor class subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F:protein tyrosine phosphatase activity; TAS
P:protein amino acid dephosphorylation; TAS
0299; Band_4.1.
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1187
1121
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716
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN-TYROSINE PHOSPHOCYSTEINE I (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FERM
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                                                                                                                 in cells
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INTERMEDIATE
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                                                                             phosphatase family.
                                                                                                                    hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                            T CELL DEVELOPMENT + H(2)0 = protein
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are no restrictions its content is in

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EMBL outstation a collaboration

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R PROSITE; PS00661; FERM 2; 1.

R PROSITE; PS00661; FERM 3; 1.

R PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

R PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

R PROSITE; PS0055; TYR_PHOSPHATASE_2; 1.

R PROSITE; PS0056; TYR_PHOSPHATASE_7; 1.

FERM.
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Best Local S
Matches 12
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InterPro; IPR000299; Band 4.1.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000242; Tyr pp.
pfam; PF00373; Band 41; I.
pfam; PF00102; Y phosphatase; 1.
prints; PR00935; BAND41.
prints; PR00935; BAND41.
prints; PR00706; PRTYPHPHTASE.
SMART; SM00295; B41; 1.
                                                                                                                                                                                                        MOUSE STANDARD; PRT; 1238 AA.

Q64455;
Q1-MOV-1997 (Rel. 35, Created)
Q1-MOV-1997 (Rel. 35, Last sequence update)
Q1-MOV-1997 (Rel. 42, Last annotation update)
Q10-CCT-2003 (Rel. 42, Last annotation update)
Q10-CCT-2003 (Rel. 42, Last annotation update)
Q10-CCT-2003 (Rel. 42, Last annotation update)
Q10-CCT-2003 (Rel. 42, Last annotation update)
Q10-CCT-2003 (Rel. 42, Last annotation update)
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Q10-CCT-2003 (Rel. 42, Last annotation update)
Q10-CCT-2003 (Rel. 35, Last sequence update)
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Q10-MOV-1997 (Rel. 35, Last
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DOMAIN
DOMAIN
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ACT_SITE
                                                                                     "Molecular cloning and characterization of Byp, a murine receptor-type tyrosine phosphatase similar to human DEP-FEBS Lett 378:7-14(1996)
                                                                                                                                    STRAIN=MRL-LPR/LPR;
MEDLINE=96140699; PubMed=8549806;
Kuramochi S., Matsuda S., Matsuda Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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PIR; JC2366;
                                                  -
                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                 NCBI_TaxID=10090;
          CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protyrosine + phosphate.
SUBCELULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed in every tissue examined.
SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
SIMILARITY: Contains 6 fibronectin type III domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               394
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SM00194; PTPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                           FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                        VHCSAGVGRTGV 1132
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635
712
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1123
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1189
1123
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639
718
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100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN-TYROSINE PHOSPHATASE.
PHOSPHOCYSTEINE INTERMEDIATE
(BY SIMILARITY).
POLY-PRO.
POLY-GLY.
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                                                                                                                                       Saitoh
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                                                                                                                                       Ohsugi M.,
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                                                                                                  DEP-1.";
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InterPro; iPR003957; FN III-like.
InterPro; iPR003957; FN III.
InterPro; iPR003961; FN III.
InterPro; iPR003387; TYR phosphatase.
InterPro; iPR000242; Tyr PP.
Pfam; PP00102; Y phosphatase; 1.
Pfam; PP00102; Y phosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00060; FN3; 6.
SMART; SM00194; PTPC; 1.
PROSITTS; PS00383; TYR PHOSPHATASE 7; 1.
PROSITTS; PS50038; TYR PHOSPHATASE 7; 1.
PROSITTS; PS50055; TYR PHOSPHATASE 7; 1.
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PROSITTS; PS50055; TYR PHOSPHATASE 7; 1. MGD; MGI:104574; Ptprj. GO; GO:0007507; P:heart development; IMP GO; GO:0001570; P:vasculogenesis; IMP. EMBL; D45212; BAA08146.1; -. PIR; S68700; S68700. P18052; 1YFO P: vasculogenesis; 1238 876 897 1238 1238 1238 114 260 348 434 518 518 518 518 CYTOPLASMIC (POTENTIAL).
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PTPU_HUMAN STANDARD; PRT; 1337 AA.

Q12913; Q15255; Q2NHM2;

Q1-NOV-1997 (Rel. 35, Created)

10-OCT-2003 (Rel. 42, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

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"In PUNCTION: May contribute to the mechanism of contact inhibit
  between
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Honda H., Inazawa J., Nishida J., Yazaki Y., Hirai H.;
"Molecular cloning, characterization, and chromosomal localization
a novel protein-tyrosine phosphatase, HPTP eta.";
Blood 84:4186-4194(1994).
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MEDIJINE-95024024; PubMed=7937872;

Oestman A., Yang Q., Tonks N.K.;

"Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced with increasing cell density.";

Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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CATALYTIC ACTIVITY: Protein tyrosine phosphate +
tyrosine + phosphate.

SUBCELLULAR LOCATION: Type I membrane protein.

PTM: N- and O-glycosylated.

DISEASE: Defects in PTPRJ are found in cancers of
                                                                 breast.
SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
SIMILARITY: Contains 5 fibronectin type III domains.
SIMILARITY: Contains 5 fibronectin type III domains.
DATABASE: NAME=PROW; NOTE=CD guide CD148 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd148.htm".
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  SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation suropean Bioinformatics Institute. There are no restrictions on its content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of t
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PROSITE; PS50055; TYR PHOSPHATASE PPP;
Signal; Glycoprotein; Transmembrane; Re
Disease mutation.
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EMBL; D37781; BAA07035.1; ---
EMBL; AF387844; AAM69432.1; ---
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R MIM; 600925; -.

R GO; GO:0005887; C:integral to plasma membrane; TAS.

R GO; GO:0005001; F:transmembrane receptor protein tyrosine pho

R GO; GO:0007267; P:cell-cell signaling; TAS.

R GO; GO:0007267; P:protein amino acid dephosphorylation; TAS.

R GO; GO:0007169; P:transmembrane receptor protein tyrosine kin

R GO; GO:0007169; P:transmembrane receptor protein tyrosine kin

R InterPro; IPR000957; FN III.

R InterPro; IPR000387; FN III.

R InterPro; IPR000387; TYP_PP.

R InterPro; IPR000242; TYP_PP.

R Pfam; PF00102; Y phosphatase; 1.

R Pfam; PF00102; Y phosphatase; 1.

R Pfam; PR000060; FN3; 8.

R SMART; SM00060; FN3; 8.

R SMART; SM00194; FN3; 8.
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MEDILINE=93180796; bubmed=8382771;

MEDILINE=93180796; bubmed=8382771;

MEDILINE=93180796; bubmed=8382771;

MEDILINE=93180796; bubmed=8382771;

MI D'Eustachio P., Morse B., Levy J.B., Laforgia S., Huebner K.,

Musacchio J.M., Sap J., Schlessinger J.;

MI Musacchio J.M., Sap J., Schlessinger J.;

MI Musacchio J.M., Sap J., Schlessinger J.;

MI Schlessinger J.;

MI Tyrosine phosphateses.";

Tyrosine phosphateses.";

Mol. Cell. Biol. 13:1497-1506(1993).

MOL Cell. Biol. 13:1497-1506(1993).

C -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = professione + phosphate.

C -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).

C -!- TISSUE SPECIFICITY: Detected in brain, lung, kidney, heart,
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/FIIa=VAR 015905.

Q -> P (in colon cancer; somatic mutation).

/FIId=VAR 015906.

G -> D (IN REF. 1).

YNGKLEPLGSYR -> LQWEAGTSGLLP (IN RI YNGKLEPLGSYR -> LQWEAGTSGLLP (IN RI MW; E6752D521C4B6AFE CRC64;
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RESULT 12
PTPG HUMAN STANDARD; PRT; 1
ID PTPG HUMAN STANDARD; PRT; 1
AC P23470; Q15623;
DT 01-FEB-1994 (Rel. 20, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence u
DT 10-OCT-2003 (Rel. 42, Last annotation
DE PTOCEAIN-TYFOSINE phosphatase gamma pr
DE gamma).
GN PTPRG.
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Pfam; PF00041; fn3; 1.
Pfam; PF00102; V_phosphatase; 2.
PF1NTS; PR00700; PRTYPHPHTASE.
PRODOM; PD000865; Euk Coanhd; 1.
SWART; SM00160; PTFC; 2.
SWART; SM00194; PTFC; 2.
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PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.

PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.

Glycoprotein; Transmembrane; Hydrolase; Repeat; Signal.

SIGNAL 1 19

BY SIMILARITY.
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PIR; B48148, B48148,
HSSP; P18052; 1YFO.
MGD; MGI:97814; Ptprg.
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PIBRONECTIN TYPE-III.
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PROTEIN-TYROSINE PHOSPHATASE 2
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"Identification of a carbonic anhydrase-like domain in the extracellular region of RPTP gamma defines a new subfamily of receptor tyrosine phosphatases", Mol. Cell. Biol. 13:1497-1506(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krueger N.X., Streuli M., Saito H.; "Structural diversity and evolution of human receptor-like protein tyrosine phosphatases."; EMBO J. 9:3241-3252(1990).
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Kaplan R., Morse B., Euebner K., Croce C., Howk R., Rave
Ricca G., Jaye M., Schlessinger J.;
"Cloning of three human tyrosine phosphatases reveals a
family of receptor-linked protein-tyrosine-phosphatases
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MEDLINE=91006018; PubMed=2170109;
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MEDLINE=96429999;
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SUBCELLURAR LOCATION: Type I membrane protein (Probable).
TISSUE SPECIFICITY: Found in a variety of tissues. It is developmentally regulated in the brain (By similarity).
SIMILARITY: Contains 1 eukaryotic-type carbonic anhydrase domains.
SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
SIMILARITY: Contains 1 fibronectin type III domain.
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1046116; AAC50439.1;
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Pfam; PF00102; Y phosphatase; 2.
Pfam; PF00102; Y phosphatase; 2.
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PROSITE; PS50055; TYR PHOSPHATASE PTP; 2
Glycoprotein; Transmembrane; Hydrolase;
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                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
CARBONIC-ANHYDRASE LIKE.
                                                                                                                                                                                                                                              N-LINKED
                                                                                                                                                                                                                                                                           SIMILARITY)
                                                                                                                                                                                                                                                                                                                              FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR POTENTIAL.
                                                                                                                                                                                                                                                            ANCESTRAL
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ne receptor protein tyrosine
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    phosphorylation; Repeat;

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    Indels
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   Gaps
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393 LVHCSAGVGRTG 404

LVHCSAGVGRTG 1068

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RESULT 13
PTP6_DROME
ID PTP6_DROME
AC P16620;
DT 01-AUG-1990
    EMBL; M27699; AAA2B842.1; -.

REMBL; M27699; B36182.

REPIR; B36182; B36182.

REMSP; P18052; 1YFO.

REMSP; P180604705; P:protein phosphatase activity; IDA.

GO; GO:00007415; P:protein amino acid dephosphorylation; IDA.

REMSP; P18008945; PM_III-like.

REMSP; P180003961; FM_III-like.

REMSP; P180003961; FM_III-like.

REMSP; P180003961; FM_III-like.

REMSP; P180003961; FM_III-like.

REMSP; P180003981; TYR_phosphatase.

REMSP; P1800041; Fn3; 3.

REMSP; P180041; Fn3; 3.

REMSP; P180041; Fn3; 3.

REMSP; P180041; Fn3; 3.

REMSP; P180048; P182; 2.

REMSP; P180048; P182; 2.

REMSP; P180049; P182; 2.

REMSP; P180049; P182; 2.

REMSP; P180049; P182; 2.

REMSP; P180049; P182; 2.

REMSP; P180049; P182; 2.

REMSP; P18005935; TYR_P180SPHATASE_7; 2.

REMSSITE; P180055; P18054; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=90046860; PubMed=2554325;
Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
"A family of receptor-linked protein tyrosine ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda, Inse
Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase DFTP precursor (
                                                                                                                SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tyrosine-phosphate phosphohydrolase).
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SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 2 fibronectin type III domains.
SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               c. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).
FUNCTION: It is possible that DPTP is a cell a
CATALYTIC ACTIVITY: Protein tyrosine phosphate
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; Immunoglobulin (
23 24 1462 P)
24 805 E:
24 805 P)
24 1462 C:
24 1462 C:
PROTEIN-TYROSINE PHOSPHATA
EXTRACELLULAR (POTENTIAL).
POTENTIAL
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
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Best Local S
Matches 12
ERRATUM.

Lee K., Nichols J., Smith A.;

Mech. Dev. 61:211-215(1996).

-!- FUNCTION: May play a role in the maintenance

-:- rom: remulated during differentiation.
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CARBOHYD
                                                                                                                                                                                                             SEQUENCE FROM N.A.

TISSUE=Embryonic stem cells;
TISSUE=Embryonic stem cells;
MEDLINE=97109513; PubMed=8951793;
Lee K., Nichols J., Smith A.;
"Identification of a developmentally regulated protein tyrosine
"Identification of a developmentally that is a marker of
phosphatase in embryonic stem cells that is a marker of
pluripotential epiblast and early mesoderm.";
Mech. Dev. 59:153-164(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P70289;
15-UTL-1998 (Rel. 36, Created)
15-UTL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Receptor-type protein-tyrosine phosphatase V precursor (EC (Embryonic stem cell protein-tyrosine phosphatase) (3S cell
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CARBOHYD
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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llarity 100.0%;
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InterPro; IPR003957; FN III-like.
InterPro; IPR003961; FN III.
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InterPro; IPR003961; TYR hosphatase.
InterPro; IPR000242; Tyr_Pr.
Pfam; PF00041; fn3; 7.
Pfam; PF00041; fn3; 7.
Pfam; PF00102; Y phosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
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PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
PROSITE; PS50055; TYR PHOSPHATASE PTP; 2.
Hydrolase; Transmembrane; Repeat; Signal;
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HSSP; P18052;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Receptor-type protein-tyrosine phosphatase V precursor (EC 3.1.3.48)
(Embryonic stem cell protein-tyrosine phosphatase) (ES cell
phosphatase) (Osteotesticular protein-tyrosine phosphatase) (OST-PTP)
PTPRV OR ESP.
                    This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come entitles requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of a hormonally regulated protein tyrosine phosphatase associated with bone and testicular differentiation.";
J. Biol. Chem. 269:30659-30667(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95074080; PubMed=7527035; Mauro L.J., Olmsted E.A., Skrobac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                epithelium.
INDUCTION: E
PTM: The cyt
                                                                                                                                                                                                                                                                                                                                                                                                         Note=No experimental confirmation available; TISSUE SPECIFICITY: Bone and testis. In the latter, restricted to the basal portion of the seminiferous tubule. DEVELOPMENTAL STAGE: Up-regulated in differentiating cultures of primary osteoblasts and down-regulated in late stage mineralizing cultures. In testis, expression is highest between stages i and then maturing spermatids remain buried within the sertoli
                                                                                                                                                                                                                                                 SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: May function in signaling pathways during bone remodeling, as well as serve a broader role in cell interaction associated with differentiation in bone and testis. Optimal pH phosphatase activity is 5.6. Associated with differentiation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine + phosphate.
SUBCELLULAR LOCATION: Type I membrane
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone and testis.

CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     osteoblasts,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comment=A presumed alternate transcript of 4.8-5.0 kilobases, which may lack PTP domains, is present in proliferating
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Contains 10 fibronectin type
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Sciurognathi; Muridae; Murinae; Rattus.
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1: sp_archea:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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## ALIGNMENTS

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Ansorge W., Wirkner U., Mewes H.W., Gassenhuber J., Wiemann is Submitted (MAY-1939) to the RMBL/GenBank/DDBJ databases.

REMBL, ALOS0040; CAB43248.1; -.

REMBL, ALOS0040; CAB43248.1; -.

RESP, Q06124; 2SHP.

RGO; GO:0016787; F:hydrolase activity; IBA.

RGO; GO:0004725; F:protein tyrosine phosphatase activity; IBA.

RGO; GO:000470; P:protein amino acid dephosphorylation; IEA.

RGO; GO:0006470; P:protein am
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Pfam; PP00102; Y_phosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00194; PTPC; 1.
PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR PHOSPHATASE_PTP; 1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
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"Expression of mouse PTP-RLIO isoforms in testis.";

Submitted (JAN.1996) to the EMBL/GenBank/DDBJ databases.

R EMBL; D83072; B8A19740.1; -.

R MGD; MGI1344406; Prepn21.

R MGD; GO:0016787; F:hydrolase activity; IEA.

R GO; GO:0016787; F:hydrolase activity; IEA.

R GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

R GO; GO:0004725; F:protein amino acid dephosphorylation; IEA.

R GO; GO:0006470; Protein amino acid dephosphorylation; IEA.

R InterPro; IPR000387; TYR_phosphatase.

InterPro; IPR000387; TYR_phosphatase.

R InterPro; IPR000387; TYR_phosphatase.

R PRINTS; PR00700; PRTYPHPHTASE.

R PRINTS; PR00700; PRTYPHPHTASE.

R PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

R PROSITE; PS00383; TYR_PHOSPHATASE_71.

R PROSITE; PS00383; TYR_PHOSPHATASE_71.

R PROSITE; PS00383; TYR_PHOSPHATASE_71.

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R PROSITE; PS0058; TYR_PHOSPHATASE_71.
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O9Y1X4;
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O1-NOV-1999 (TrEMBLrel. 2
O1-JUN-2003 (TrEMBLrel. 2
SPTPR5 (Fragment)
SptPR5 (Fragment)
Ephydatia fluviatilis.
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PROSITE; PS50055; TYR. I
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Q1-MAY-2000
                        NCBI_TaxID=31330
                                                                Bukaryota; Metazoa; Porifera;
Haplosclerida; Spongillidae;
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STRAIN=C57-BL6; TISSUE=Testis;
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Mammalia; Eutheria;
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PS50055; TYR_PHOSPHATASE_PTP;
ical protein; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLIVHCSAGVGRTGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNRYRDILPYDSTRVPLGK 247
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(TrEMBLrel.
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llarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Rođentia;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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2.3e-
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RC STRAIN=CZECH II; TISSUE=Breast tumor;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RX Strausberg R.L., Feingold E.A., Grouse L.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsish F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsish F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Uddin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

RA Bramstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Arzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J. MWATAM M...
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Matches
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R GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

R GO; GO:00044725; F:protein mino acid dephosphorylation; IEA.

R InterPro; IPR000387; TYR phosphatase.

R InterPro; IPR000382; Tyr Pp.

R Pfam; PF00102; Y phosphatase; 2.

R Pfam; PF00102; Y phosphatase; 2.

R PRINTS; PR00770; PRTYPHPHTASE.

R SMART; SM00194; PTPC; 2.

R PROSITE; PS00383; TYR PHOSPHATASE 1; 1.

R PROSITE; PS00383; TYR PHOSPHATASE 2; 2.

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HSSP; P18052; 1YFO.
GO; GO:0016787; F:hy
GO; GO:0004725; F:pr
GO; GO:0006470; P:pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7TMG1;
SEQUENCE FROM N.A. STRAIN=CZECH II; I Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                 oones S.J., Marra M.A.;
"Generation and initial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ono K., Suga H., Iwabe N., Kuma K., Miyata T.;
"Multiple protein tyrosine phosphatases in sponges and explosive gene duplication in the early evolution of animals before the parazoan-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eumetazoan split. ";
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MEDLINE=99246376; PubMed=10229569;
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                                                                                                                                                             mouse
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15; Conservative
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                                                                                                                                                          CDNA
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                                                                                                                                                          and initial analysis of more than 15,000 DNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48:654-662(1999).
7; BAA82560.1; -.
                                       TISSUE=Breast tumor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1
50365 MW;
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PRELIMINARY;

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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence up
01-UUN-2003 (TrEMBLrel. 24, Last annotation
Protein tyrosine phosphatase rPTP-GMC1 (Frag

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NON TER
SEQUENCE
                                                                                                                                                                                                            Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL353786; CAD19000.1; -.
CO:0005856; CAD19000.1; -.
CO:0005856; C:Qytoskeleton; IEA.
GO:0004725; P:protein tyrosine phosphatase activity;
GO:0004725; P:protein tyrosine phosphatase activity;
GO:0004872; P:receptor activity; IEA.
GO:0006470; P:protein amino acid dephosphorylation;
InterPro; IPR00029; Band 4.1.
InterPro; IPR00029; Band 4.1.
InterPro; IPR00029; Tyr.Dosphatase.
InterPro; IPR000242; Tyr.Dp.
                                                                                                                   PROSITE; PS00661; FERM_2; 1.

PROSITE; PS00187; FERM_3; 1.

PROSITE; PS00181; TYR_PHOSPHATASE_1; 1.

PROSITE; PS00185; TYR_PHOSPHATASE_2; 1.

PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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ne phosphatase, non-receptor type
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Pred. No.
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dephosphorylation; IEA.
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9.2e-07
                                                                  DB 4;
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MGD; MGI:1096349; Ptprq.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0004721; F:protein phosphatase activity; IEA.

GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

InterPro; IPR001087; TYR phosphatase.

PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
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SEQUENCE FROM N.A.

MEDITINE-98395110; PubMed=9727007;

Wright M.B., Hugo C., Seifert R., Disteche C.M., Bowen-Pope D.F.;

"Proliferating and migrating mesangial cells responding to injury
express a novel receptor protein-tyrosine phosphatase in experimental
mesangial proliferative glomerulonephritis.";

J. Biol. Chem. 273:33999; Janc34823.1; -.

EMBL; AP073999; AAC34823.1; -.
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MEDIINE-98395111; PubMed=9727007;
Wright M.B., Hugo C., Seifert R., Disteche C.M., Bowen-Pope D.F.;
"Proliferating and migrating mesangial cells responding to injury
express a novel receptor protein-tyrosine phosphatase in experimental
mesangial proliferative glomerolonephritis.";
J. Biol. Chem. 273:23929-23937(1998).
EMBL; ABC973998, ABC348822.1; -.
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GO; GO:0004721; F:protein phosphatase activity;
GO; GO:0006470; F:protein amino acid dephosphory
InterPro; IPR000387; TYR phosphatase.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_FHOSPHATASE_2; 1.
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Mammalia; Eutheria;
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SEQUENCE FROM N.A.
STRAIN=C5-PBL/6J; TISSUE=Diencephalon;
STRAIN=C2354683; PubMed=12466851;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research G
*Analysis of the mouse transcriptome ba
60,770 full-length cDNAs.*;
Nature 420:563-573(2002).
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QBCC23;
Q1-MAR-2003
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Unknown EST
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PRINTS; PRO0700; PRTVEHENTALE.

SMART; SM00404; PTPC motif; 1.

PROSITE; PRO0383; TYR PHOSPHATASE 1; 1.

PROSITE; PS50056; TYR PHOSPHATASE 2; 1.

PROSITE; PS50055; TYR PHOSPHATASE TP;
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GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
InterPro; IPR003595; PTPc motif.
InterPro; IPR0003595; PTPc motif.
InterPro; IPR0003597; TYR phosphatase.
InterPro; IPR000242; Tyr PP.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
                                                                                                                                                                                                                   Eukaryota, Metazoa,
Mammalia, Eutheria,
                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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EMBL; AX034067; BAC28569.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome 60,770 full-length CDNAs.";
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Mammalia; Eutheria;
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Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 1.4e-06;
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Q9UMZ3;
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SEQUENCE
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GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000242; TYR-PP.
Pfam; PF00102; Y_bhosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
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"Differential expression of PTPase RNAs resulting differentiation induced by PMA,";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ data EMBL; AP169351; AAD50277.1;
                                                                                                                                                                                                                                                                  SMART; SM00194; PTPC; 1.

PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.

PROSITE; PS50056; TYR_PHOSPHATASE 2; 1.

PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
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GO; GO:000470; F:protein amino acid dephosphorylation; IEA.
InterPro; IPR00395; PTPC motif.
InterPro; IPR00397; TYR_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
Pfam; PF00102; Y:phosphatase; 1.
Pfam; PF00102; Y:phosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00404; PTPC_motif; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_2; 1.
PROSITE; PS00385; TYR_PHOSPHATASE_PTP; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MGI:97812;
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NON TER
SEQUENCE
EMMBL, AK042201; BAC31488.1; -.

MGD; MGI:97812; Ptprd.

GO; GO:0004725; Fiprotein tyrosine phosphatase activity; IEA

GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

InterPro; IPR003595; PTPC motif.

InterPro; IPR003597; TYR_phosphatase.

InterPro; IPR003242; Tyr_PP.
                                                                                                                                                                                                                                           the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o 60,770 full-length cDNAs.";
Mature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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MEDLINE=99246376; PubMed=10229569;

Ono K., Suga H., Iwabe N., Kuma K., Miyata T.;

Ono K., Suga H., Iwabe Dosphatases in sponges and explosive nutiple protein tyrosine phosphatases in sponges and explosive duplication in the early evolution of animals before the parazoar
                                                                                                                                                                                                                                                                                                                                                                                     The FANTOM Consortium,
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PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
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GO; GO:0004725; F:protein tyrosine phosphatase activity;
GO; GO:0006470; P:protein amino acid dephosphorylation; InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000242; Tyr_PP.
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Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
Haplosclerida; Spongillidae; Ephydatia.
NCBI_TaxID=31330;
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01-NOV-1999 (TREMBLICE)
01-JUN-2003 (TREMBLICE)
SPTPR3 (Fragment)
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HSSP; P18052; 1YFO.
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R GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
R GO; GO:0004872; F:receptor activity; IEA.
R GO; GO:0004870; P:protein anino acid dephosphorylation; IEA.
R InterPro; IPR000387; TYR_phosphatase.
R InterPro; IPR000242; Tyr_PP.
R Pfam; PF00102; Y phosphatase; 2.
R PRINTS; PR00700; PRTYPHPTASE.
R PRINTS; FR00700; PRTYPHTASE.
R PRINTS; PS001383; TYR_PHOSPHATASE_1; 2.
R PROSITE; PS00383; TYR_PHOSPHATASE_7; 2.
R PROSITE; PS0035; TYR_PHOSPHATASE_PTP; 2.
R PROSITE; PS0035; TYR_PHOSPHATASE_PTP; 2.
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PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM000194; PTPC; 1.
SMART; SM000404; PTPC motif; 1.
SMART; SM000404; PTPC motif; 1.
PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
PROSITE; PS00356; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                Hydrolase;
SEQUENCE
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01-NOV-1996 (TrEMBLrel. 01, Last sequence
01-JUN-2003 (TrEMBLrel. 24, Last annotatic
LAR receptor-linked tyrosine phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U00477; AAC04306.1; -. PIR; A56493; A56493.
HSSP; P18052; 1YFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Leukocyte common antigen-related receptor-linked tyrosine phosphatase. Regulation of mRNA expression."; J. Biol. Chem. 268:26503-26511(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Sprague Dawley; TISSUE=Brain; MEDLINE=94075340; PubMed=8253779;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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Brosius J.;
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HSSP; P18052; 1YFO.
GO: GO:0016787; F:hydrolase activity; IEA.
GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
GO; GO:000470; P:protein amino acid dephosphorylation; IEA.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000387; TYR PP.
Pfam; PF00102; Y_phosphatase; 2.
PRINTS; PR001700; PRTYPHPHTASE.
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MEDLINE=20219325; PubMed=10754074;
Ono-Koyanegi K., Suga H., Katoh K., Miyata T.;
"Protein tyrosine phosphatases from amphioxus,
"Protein tyrosine phosphatases from amphioxus,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii, Squalea; Hypnosqualea; Pristiorajea; Batcidea;
Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.
NCBI_TaxID=86373;
                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                 Hydrolase.
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PROSITE; PS00383; TYR PHOSPHATASE 1; 2.
PROSITE; PS50056; TYR_PHOSPHATASE_PTP;
PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
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SMART; SM00194;
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